Title: Perfect score: Sequence:

US-09-846-512-12 2447 1 MGENDPPAVEAPFSF

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Scoring table:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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RESULT 1
TMS3_HUMAN
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P57727;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
TRANSMEMBRANE PROTEASE, SERINE 3 (EC 3.4.21.) (SERINE PROTEASE
TADG-12) (TUMOR ASSOCIATED DIFFERENTIALLY-EXPRESSED GENE-12 PROTEIN).
TMPRSS3 OR TADG12 OR ECHOS1.
Homo sapiens (Human).
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44444333354
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                                                                                                                                                                                                                                                                                                                                                                                                                           protease causing both congenital recessive deafness.";
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MEDLINE=20521358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Ovarian
                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                         FUNCTION: PROBABLE PROTEASE.

SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).

ALTERNATIVE PRODUCTS: 4 ISOFORMS; A (SHOWN HERE), B/C, D AND TRUNCATED/TAGG-12Y; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES. THE TRUNCATED ISOFORM IS FOUND AT INCREASED LEVELS IN SOME CARCINOMAS.

DISEASE: DEFECTS IN TWARSS3 ARE A CAUSE OF TWO FORMS OF AUTOSOMAL NEUROSENSORY CHILDHOOD-ONSET FORMS OF DEAFNESS, DENB8 AND DENB10.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                SIMILARITY: CONTAINS 1 SRCR DOMAIN. SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
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          non-profit institutions as long land this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
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Match

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Query

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TMS2_HUMAN
TMS5_MOUSE
TMS5_HUMAN
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TMS3_HUMAN

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ST14_HUMAN
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NETR_MOUSE
PLMN_HORSE

KAL_MOUSE

KAL_RAT

HEPS_MOUSE HEPS_RAT

ENTK_PIG ENTK_HUMAN

CORI_MOUSE
PLMN_HUMAN
MCT7_MOUSE
ACRO_MOUSE

PLMN_SHEEP PLMN_ERIEU

CORI_HUMAN
ST14_MOUSE
TEST_HUMAN
PLMN_MOUSE
ACRO_RAT

Database

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SwissProt_39:*

Post-processing: Minimum Match

Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

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AF201380; AB038157; AB038158;

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Query Match
Best Local Similarity
Matches 454; Conserv
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SMART; SM00202; SR; 1.

SMARR; SM00202; SR; 1.

SMARR; SM00202; TYP_SPC; 1.

SMO0202; TYP_SPC; 1.

PROSITE; PS01209; LDLRA_1; 1.

PROSITE; PS09020; BCRLA; FALSE_NEG.

PROSITE; PS00287; SRCR_2; 1.

PROSITE; PS00240; TRYPSIN_DOM; 1.

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InterPro;
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IPR001254; Tryps
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49404 MW;
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LDL_recept_A.
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8 CYTOPLASMIC (POTENTIAL).

9 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                  SERRINE PROTEASE.

SERRINE PROTEASE.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHEAVAGE (POTENTIAL).

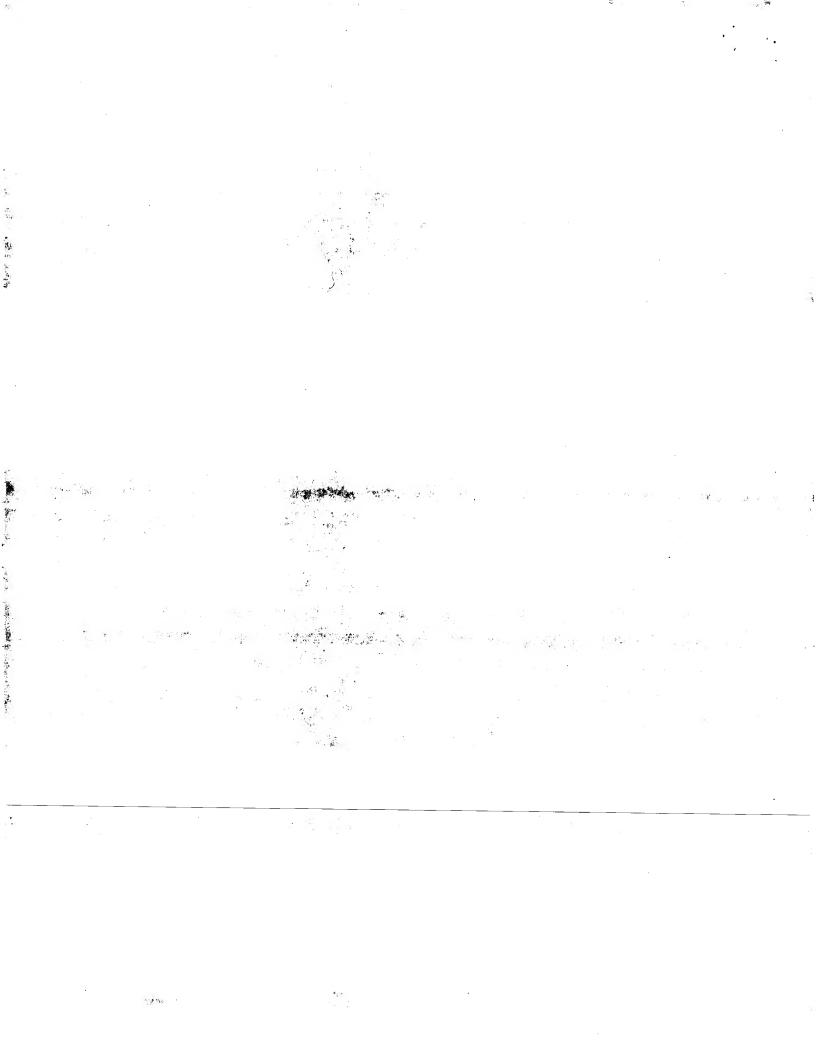
BY SIMILARITY.

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V -> I.
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                                                                    LKFFPIIVI -> FEVFSQSSSL (IN REF. 1).
A -> T (IN REF. 1).
MISSING (IN REF. 1).
ICHRDVYGGIISPSMLCAGYLTGGVD -> DLQPQGRVRW
HHLPLIALIGLDGWRRN (IN REF. 1).
E -> D (IN REF. 1).
; 57ECC3678E7D6AFF CRC64;
 Score 2447; DB 1;
Pred. No. 6.9e-201;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
LDL-RECEPTOR CLASS A.
                                                                                                                                                                                                                                             EAFL (IN ISOFORM D).
DLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYH
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SEQUENCE FROM N.A. STRAIN-BALE/C; STRAIN-BALE/C; Jacquinet E.J., Rao N.V., Rao G.N., Holdal J.R.; A novel mosaic serine protease, epitheliasin."; Submitted (DEC-1998) to the EMBL/GenBank/DBDJ databases. -! SUBCLELULIAR ICCATION: TYPE II MEMBRANE PROTEIN. -! TISSUE SPECIFICITY: EXPRESSED MAINLY IN PROSTATE AND KIDNEY. -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. -! SIMILARITY: CONTAINS 1 SRCR DOMAIN. -! SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.	SEQUENCE FROM N.A. Han J., Kim S.; "Putative transmembrane protease X."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. [3]	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY. STRAIN-BALB/C; MEDLINE-21104370; PubMed-11169526; Waarala M.H., Porvari K.S., Kellokumpu S., Kyllonen A.P., Vihko P.T.; "Expression of transmembrane serine protease TMPRSS2 in mouse and human tissues."; J. Pathol. 193:134-140(2001).	Mus musculus (Mouse). Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;	TMS2_MOUSE STANDARD; PRT; 490 AA. Q9JI08; Q9JKC4; Q9QV82; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) TRANGMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21:-) (EPITHELIASIN) (PLASMIC TRANGMEMBRANE PROTEIN X).	421 FG ULT 2 2_MOUSE	21 FGIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT 454	361 AVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATS 420 	301 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLNHA 360 	241 LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLYSLLDNPAPSHLVEKIVYHSKYKPKR 300 	181 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH 240 	121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180 	61 LALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF 120 	1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI 60

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Ferrara N, Filvaroff E,
Goddard A, Godowski PU,
Kljavin IJ, Kuo SS, Napi
Shelton DL, Stewart TA,
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30-DEC-1999;
05-JAN-2000;
06-JAN-2000;
06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                c78458 to c78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides have cytostatic activity to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. C78600 to C78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel PRO polypeptides and polynucleotides used i to target bioactive molecules to specific cells, cellular activities -
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99WO-US31274.
2000WO-US00219.
2000WO-US00277.
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E, Fong S, Gao W, Gerber H, Gerritsen PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA;
TA, Tumas D, Williams PM, Wood WI;
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Pred. No. 2.6e-188;
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Copyright (c) 1993 - 2000 Com
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US-08-508-448C-19
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US-08-94-83-65
US-08-94-83-65
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US-08-248-629A-1
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Cal Simi: 444; 444; MGENDPPI HILALAIGI ILALAIGI	1 -046-2 -046-2 -046-3 INFORMATION: ANT: O'Brien, ANT: O'Brien, ANT: Underwooder INVENTION: DEFINVENTION: EFFERNCE: DEFERENCE: DATE RAPPLICATION T FILING DATE R APPLICATION T FILING DATE RESE: HOTORNATION: INFORMATION: INFORMATION: -046-2	
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197.6 tive	ion US/09518046 Timothy J. Timothy J. G. Lowell J. Transmembrane In Ovarian Car 2000-03-02 NUMBER: US/09/ : 2000-03-03 S: 153 S: 153 iens complete amino protein	812 812 812 812 812 814 791 791 790 790 791 791 791 810 810 810
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	\$18046 J. J. Carcinema 15/09/518,04 02 02 02 03 amino acid	US-08- US-08- US-08- US-08- US-08- US-08- US-08- US-08- US-09- US-09- US-09- US-09- US-09- US-09- US-09- US-08- US
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RESULT 2
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APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
FILE REFERENCE: D6192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Amino acid sequence of TADG-12 encoded by nucleotides OTHER INFORMATION: 144 to 1511 of Sequence 1 Patent No. 6291663 5-99-261-416-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/261,416A CURRENT FILING DATE: 1999-03-03 NUMBER OF SEQ ID NOS: 14
SEQ ID NO 2
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Best Local Similarity
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TYPE: PRT
ORGANISM: Homo sapiens
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416
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                                                                                                                                                                                                                                                                                                                                                                                                             ILALAIGLGIHFDCSGKYRCRSSFKCIELITRCDGVSDCKDGEDEYRCVRVGGQNAVLQV 120
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91.5%;
                                                               -GRVRWHHLPLHALRGLPDGWRWNSCQGDSGGPLVCQERRLWK 415
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Pred. No. 6e-207;
5; Mismatches 23;
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GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
FILE REFERENCE: D6192CIP
CURRENT APPLICATION NUMBER: US/09/518,046
CURRENT FILING DATE: 2000-03-02
EARLIER APPLICATION NUMBER: 09/261,416
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 4
LENGTH: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: complete amino acid
; OTHER INFORMATION: variant protein
US-09-518-046-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-09-342-749-2
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                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
APPLICANT: Tavtidian, Sean V.
APPLICANT: Teng, David H.-F.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor
FILE REFERENCE: 2318-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09518046 Patent No. 6294663
                                                                                           SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09342749 Patent No. 6166194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 258; Conserv
                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/342, 749
CURRENT FILING DATE: 1999-66-29
EARLIER APPLICATION NUMBER: US 60/091, 044
EARLIER FILING DATE: 1998-06-29
ORGANISM: Homo sapiens -09-342-749-2
                                                                                                               NUMBER OF SEQ ID NOS: 33 SOFTWARE: PatentIn Ver.
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TYPE: PRT
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                                            TYPE: PRT
                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 HLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSL------LDNPAPSH 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 KVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQMPMQASLQFQGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ILALAIGLGIHFDCSGKYRCRSSFKCIELITRCDGVSDCKDGEDEYRCVRVGGQNAVLQV 120
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                                                                  4.92
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Pred. No. 9.7e-125;
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120 CNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVC 157

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; OTHER INFORMATION: protease
US-09-518-046-23
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                                                                                                                                                             Query Match
Best Local Similarity
Matches 157; Conserv
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Patent No. 6294663
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/518,046 CURRENT FILING DATE: 2000-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Transmembrane Serine TITLE OF INVENTION: in Ovarian Carcinoma
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 153
EQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 09/261,416 EARLIER FILING DATE: 1999-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: D6192CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: O'Brien, Timothy J. APPLICANT: Underwood, Lowell J.
                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                 ENGTH: 157
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               370
                                                         310 LAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLNHAAVPLISNKI 369
                                                                                                                   250 LWIITAAHCYYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMK 309
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              CNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVC
                                                                                                     LWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMK
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                                          LAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDG-GDASPVLNHAAVPLISNKI
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Application US/09518046
                                                                                                                                                                Conservative
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                                                                                                                                                                           Score 851.5; DB Pred. No. 7e-76;
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                                                                                                                                                                                           DB 4;
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Matches
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Patent No. 6043033
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 415-855-05:
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED
TITLE OF INVENTION: PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
419 TSFGIGCAEVNKPGVYTRVTSFLDWIHEQMERD
                                                                                                                                                                                                                                                                                                                                                                                                                                                MMEDILL
LIBRARY: SUC
TONE: 556016
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                                                                                                                               131
                                                         190
                                                                                                                                                                   299
                                                                                                                                                                                                                                            242
                                                                                                                                                                                                                                                                                                               184 LHHSVYVREGCASGHVVTLQCTACGHRRGYS--SRIVGGNMSLLSQWPWQASLQFQGYHL 241
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                                                                                                                                                                                                                                                                              12 IYKKLYHSDACSSKAVVSLRCIACGVNLNSSRQSRIVGGESALPGAWPWQVSLHVQNVHV 71
                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/8 FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                             CGGSVITPLWIITAAHCV-YDLYLPKSWTIQVGLV--SLLDNPAPSHLVEKIVYHSKYKP 298
                                                         AAKVLLIETQRCNSRYVYDNLITPAMICAGFLQGNVDSCQGDSGGXLVTSKNNIWWLIGD 249
                                                                                       HAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGA 418
                                                                                                                                                                                                      CGGSIITPEWIVTAAHCVEKPLNNPWHWTAFAGILRQSFMFYGA-GYQVEKVISHPNYDS 130
                                                                                                                               KTKNNDIALMKLQKPLTFNDLVKPVCLPNPGMMLQPEQLCWISGWGATEE-KGKTSEVLN 189
                                                                                                                                                    KRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLN 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 amino acids
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                                                                                                                                                                                                                                                                                                                                                                  28.1%; Score 686.5; 50.2%; Pred. No. 2.4
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2.4e-59;
92;
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                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                           196
                                                                 135
                                                                                                   139 NVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHHSVYVREG---CA 195
                                                                                                                                               75
                                                                                                                                                                                   92 CDGVSDCKDGEDEYRC-----VRVGGQNAVLQVFTAA--SWKTMCSDDWKGHYA 138
                                                                                                                                                                                                                         22 IPMETFRKVGIPIIIALLSLASIIIVVVLIKVILD---KY----YFLCGQPLHFIPRKQL 74
                                                                                                                                                                                                                                                                 44 LPLKFFPIIVIGIIALILALA-----IGLGIHFDCSGKYRCRSSFKC---IELIAR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/008,271A FILING DATE: 16-Jan-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HUMAN PROTEASE MOLECULES NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM
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Hillman, Jenn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                           CDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALA 134
                       SGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITA 255
                                                             ETACRQMGYSS------KPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPCL 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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Corley, Neil C.
Tang, Tom Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shah, Purvi
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                                                                                                                                                                                                                                                                                                       27.0%; Score 660.5; DB 4; 35.4%; Pred. No. 1.6e-56; tive 73; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jennifer L.
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    Length 435;
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                                                                                                                                                                                             Matches 146;
                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 876-58 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170 X8574
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                     474 IQSIWHVACAENWTTQISDDVCQLLGLGT--GNSSVPTFSTGG---GPYVNLN----- 521
                                                                          121 TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 KPGVYTRVTSFLDWIHEQMERDL 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 AHCV---YDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIV---YHSKYKPKRLGNDIALMK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 SGSLVSLHCLACGESL-KTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 241
181 VTALHHSVYV--REGCASGHVVTLQCT--ACGHR---RGYSSRIVGGNMSLLSQWPWQAS 23
                                                                                                                                 66 GLGIHFDC-SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRV----GGQNAVLQVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meinert, Maureen C. REGISTRATION NUMBER: 31,544 REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 23
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                   GLGIPEPCKEDNFQCKDG-ECIPLVNLCDGFPHCKDGSDEAHCVRLFNGTTDSSGLVQFR 473
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N: 435
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36.9%;
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                                                                                                                                                                                                                Score 660; DB 1; Length 798; Pred. No. 4.3e-56;
                                                                                                                                                                                             Mismatches 146;
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                                                                                                                                                                                             Indels 34;
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PCT-US94-00616-2
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PCT-US94-00616-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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TYPE: a
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    700
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                              66 GLGIHFDC-SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRV----GGQNAVLQVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                        VTALHHSVYV--REGCASGHVVTLQCT--ACGHR---RGYSSRIVGGNMSLLSQWPWQAS 233
                                                                                                                                                                                                                                                                                                                                                     TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDK 180
                                                                                                                                                                                                                                                                                                                                                                                            GLGIPEPCKEDNFQCKDG-ECIPLVNLCDGFPHCKDGSDEAHCVRLFNGTTDSSGLVQFR 473
                      AGDASPVLNHAAVPLISNKICNHR-DVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQ 408
QGSTADVLQEADVPLLSNEKCQQQMPEYN--ITENMVCAGYEAGGVDSCQGDSGGPLMCQ
                                                                           IVINPHYNKRRKNNDIAMMHLEMKVNYTDYIQPICLPEENQVFPPGRICSIAGWGAL-IY 699
                                                                                                 IVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDG
                                                                                                                                                      LYFDDQQVCGASLVSRDWLVSAAHCVYGRNMEPSKWKAVLGLHMASNLTSPQIETRLIDQ
                                                                                                                                                                            LQFQGYHLCGGSVITPLWIITAAHCVYDLYL-PKSWTIQVGL--VSLLDNP-APSHLVEK 289
                                                                                                                                                                                                                                   -TAPNGSLILTPSQQCLEDSLILLQCNYKSCGKKLVTQEVSPKIVGGSDSREGAWPWVVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGSTADVLQEADVPLLSNEKCQQQMPEYN--ITENMVCAGYEAGGVDSCQGDSGGPLMCQ
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36.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 660; DB 5; Length 798
Pred. No. 4.3e-56;
0; Mismatches 146; Indels
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; Sequence 2, Application US/09000846
; Patent No. 5981830
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US-09-000-846-2
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Best Local Similarity
Matches 143; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 703-243-6410 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,846
FILING DATE: 30-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WU, QINGYU
APPLICANT: SADLER, JASPER
TITLE OF INVENTION: KNOCKOUT MICE AND THEIR PROGENY
TITLE OF INVENTION: DISRUPTED SERINE PROTEASE GENES
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
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APPLICATION NUMBER:
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                         318
                                                                                                                                              155
                                                                                                                                                                                                                          105 VRTAGANGTSGFFCVDEGGLRLAQRLL--DVISVC------DCPRGRFLTATCQDCGR 154
                                                                                                                                                                                                                                                                    158
                                                                                                                                                                                                                                                                                                                                              100 DGEDEYRCVRVGGQNAVLQVF--TAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLR 157
                                                                                                      267
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                                                                                                                                                                                                                                                                                                            46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: LEBOVITZ, RICHARD M.
REGISTRATION NUMBER: 37,06
REFERENCE/DOCKET NUMBER: E
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ZIP: 22201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADUKESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C. STREET: 2200 CLARENDON BLVD. SUITE 1400 CITY: ARLINGTON STATE. ...
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EMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLNHAAVPLISNKICNHRDVYG
                                                            VLSRWRVFAGAVARTSPHAVQLGVQAVIYHGGYLPFRDPTIDENSNDIALVHLSSSLPLT 269
                                                                                                                                                                                                                                                                VSSLEGQFREEFVSID------HLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGH 209
                                                                                                                                                                                                                                                                                                        DQEPLYQ-VQLSPGDSRLAVFDKTEGTWRLLCSSRSNARVAGLGCEEMGFLRALAHSELD 104
                                                                                                    ---SWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR-----LGNDIALMKLAGPLTFN 317
                                                                                                                                            RKLPVDRIVGGQDSSLGRWPWQVSLRYDGTHLCGGSLLSGDWVLTAAHC-----FPERNR 209
                                                                                                                                                                        RRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPK--- 266
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US-08-944-483-67; Sequence 67, Application US/08944483; Patent No. 6232456; Patent No. 6232450
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; OTHER INFORMATION:
US-09-027-337-3
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LENGTH: 256
TYPE: PRT
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Best Local Similarity 45.1%;
Matches 114; Conservative 3
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APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/027,337B CURRENT FILING DATE: 1998-02-20
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                                                                                                     APPLICANT:
APPLICANT:
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                    APPLICANT:
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                                                                                                                                                                                                                                                                                                           VTSFLDWIHEQME 449
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 S.
 INVENTION:
                                                                                     COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GRANADOS, EDWARD N.
                                 KLASS, MICHAEL R. RUSSELL, JOHN C. STEWART, KENT D.
                                                                                                                                          COHEN, MAURICE
                  STROUPE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serine protease catalytic domain homologous to similar domain in T
NOVEL SERINE PROTEASE
                  STEVEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           %; Score 576; DB 2;
%; Pred. No. 1.4e-48;
37; Mismatches 74
 REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 256
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TADG-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                171
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RESULT 13
US-08-681-151-3
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                                                        Sequence 3, Application US/08681151 Patent No. 5869637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                  GENERAL INFORMATION:
APPLICANT: Au-You
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: AN TITLE OF INVENTION: OF NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
  APPLICANT:
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                                                                                                                                                                                                                 438 TSFLDWIHEQME 449
                                                                                                                                                                                                                                                         172
                                                                                                                                                                                                                                                                                                                                                                     322 PVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLNHAAVPLISNKICNHRDVYGGIIS 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                    271
                                                                                                                                                                            232
                                                                                                                                                                                                                                                                                                                                 113 PVCLPAAGQALVDGKICTVTGWGNTQ-YYGQQAGVLQEARVPIISNDVCNGADFYGNQIK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 IVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPK-----SWTI 270
                                                                                                                                                                                                                                                                                                                                                                                                           56 FAGAVA---QASPHGLQLGVQAVVYHGGYLPFRDPNSEENSNDIALVHLSSPLPLTEYIQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    QVGLVSLLDNPAPSHL---VEKIVYHSKYKPKR-----LGNDIALMKLAGPLTFNEMIQ 321
                                                                                                                                                                          SDFREWIFQAIK 243
                                                                                                                                                                                                                                                                                           PSMLCAGYLTGGVDSCQGDSGGPLVCQE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVGGRDTSLGRWPWQVSLRYDGAHLCGGSLLSGDWVLTAAHC-----FPERNRVLSRWRV 55
                                                                                                                                                                                                                                                       PKMFCAGYPEGGIDACQGDSGGPFVCEDSISRTPRWRLCGIVSWGTGCALAQKPGVYTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abbott Park
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ilarity 44.8%;
Conservative 3
Bandman,
                    Au-Young,
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                    Janice
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; Pred. No. 4.4e-48;
37; Mismatches 74;
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                                                                                                                                                                                                                                                                                         RRLWKLVGATSFGIGCAEVNKPGVYTRV 437
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APPLICANT:

Braxton, Scott Michael

COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

COUNTRY:

Sn

Palo Alto

CA

94304

OPERATING SYSTEM:

IBM Compatible

Diskette

CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,

3174 Porter Drive

APPLICANT: GOli, SUTYA
TITLE OF INVENTION: A NOVEL HUMAN KALLIKREIN
NUMBER OF SEQUENCES: 4

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RESULT 14
US-08-508-448C-25
Sequence 25, Application US/08508448C
Patent No. 5804410
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Best Local Similarity
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 205011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           189 YVREGCASGHVVTL------QCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQ----G
                                                                                                                                                  415
                                                                                                                                                                                   535
                                                                                                                                                                                                                    357
                                                                                                                                                                                                                                                     476
                                                                                                                                                                                                                                                                                    297
                                                                                                                                                                                                                                                                                                                       416
                                                                                                                                                                                                                                                                                                                                                     239 YHLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSL--LDNPAPSHLVEKIVYHSKY 296
                                                                                                                                                                                                                                                                                                                                                                                      362 YEAQG-SSGYSLRLCKVVESSDCTT-----KINARIVGGTNSSLGEWPWQVSLQVKLVSQ 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                 LVGITSWGEGCARKEQPGVYTKVAEYIDWILEKIQSSKERALET 635
                                                                                                                                             LVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQM----ERDLKT 454
                                                                                                                                                                                 LQKATIPLVPNEECQKKYRDY---VITKQMICAGYKEGGIDACKGDSGGPLVCKHSGRWQ
                                                                                                                                                                                                                                                                                                                    NHMCGGSIIGRQWILTAAHCEDGIPYPDVWRIYGGILNLSEITNKTPFSSIKELIIHQKY
                                                                                                                                                                                                                  LNHAAVPLISNKIC--NHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWK 414
                                                                                                                                                                                                                                                  {\tt KMSEGSYDIALIKLQTPLNYTEFQKPICLPSKADTNTIYTNCWVTGWGYTKE-RGETQNI}
                                                                                                                                                                                                                                                                                 KPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 570; DB 2;
Pred. No. 2.1e-47;
2; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                          88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kazuyoshi YAMAOKA et al.
TITLE OF INVENTION: NUCLEIC ACID SE
TITLE OF INVENTION: TRYPSIN-LIKE EN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Wordperfect 5:1 CURRENT APPLICATION DATA:
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361
                                    394
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                                                                                                                                                                                                                                                                                                                                                                                                                          107 CVRVGGQNAVLQVFTAASWKTM------CSDDWKGHYANVACA-QLGFPSYVSSDNLR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US FILING DATE: July 28, CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V Match 23.1%; Score 564.5; DB 1;
Local Similarity 34.2%; Pred. No. 3.9e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
SOFTWARE: Wordper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                          75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 IIVIGIIALILALAIGLGIHFDC--SGKYRCRSSFKC--IELIARCDGVSDCKDGEDEYR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP:
                                                                                                                                                                                                                                                                 SSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVG
VDACQGDSGGPLVQEDSRRLWFIVGIVSWGDQCGLPDKPGVYTRVTAYLDWIRQQ 415
                                                                                                 DGKVCWTSGWGATEDGAGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGG
                                                                                                                                                     ISTTF - - PKLRMRVRNILIHNNYKSATHENDIALVRLENSVTFTKDIHSVCLPAATQNIP
                                                                                                                                                                                          LVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFP 333
                                                                                                                                                                                                                              EQRILGGTEAEEGSWPWQVSLRLNNAHHCGGSLINNMWILTAAHCFRSNSNPRDWIATSG
                                                                                                                                                                                                                                                                                                             IESVLRQMLNNSGNLE-INPSTEITSLTDQAAANWLINECGAGPDLITLS---
                                                                                                                                                                                                                                                                                                                                                  VSSLEGQFREEFVSIDHLLPDDKVTALHHSV---YVREGCASG-HVVTLQCTACGHRRGY 213
                                                                                                                                                                                                                                                                                                                                                                                        TLSGRIESLITKTFKESNLRNQFIRAHVAKLRQDGSGVRADVVMKFQFTRNNNGASMKSR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVVAGVV--ILAVTIALLVYFLAFDQKSYFYRSSFQLLNVEYNSQLN----SPATQEYR
                                VDSCQGDSGGPLVGQE-RRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQ 447
                                                                          PGSTAYVTGWGA-QEYAGHTVPELRQGQVRIISNDVCNAPHSYNGAILSGMLCAGVPQGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Wenderoth, Lind & I
805 Fifteenth Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68; Mismatches 166;
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RESULT 15
US-08-508-448C-19
; Sequence 19, Applicatio
; Patent No. 5804410
; GENERAL INFORMATION:
Search completed: April 11, 2002, 08:53:24
Job time: 52 sec
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US-08-508-448C-19
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 21.8%; Score 533; DB 1; Length 232; Best Local Similarity 45.7%; Pred. No. 2e-44; Matches 106; Conservative 32; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: WAZTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/
FILING DATE: July 28, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KAZUYOShi YAMAOKA et al.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING
TITLE OF INVENTION: TRYPSIN-LIKE ENZYME AND PROCESS FOR PRODUCING THE ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                             119 TAYYTGWGA-QEYAGHTVPELRQGQVRIISNDVCNAPHSYNGAILSGMLCAGVPQGGVDA 177
                                                                                                                                                                                                277 LLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGK 336
                                                                                                                                                                                                                                                                                                                                                                 217 IVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS: sir TOPOLOGY: linear
                                                                                                                                                                                                                                                  61 TF--PKLRMRVRNILIHNNYKSATHENDIALVRLENSVTFTKDIHSVCLPAATQNIPPGS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 amino acids
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805 Fifteenth Street, N.W., #700
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Title:
Perfect score:
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2447
1 MGENDPPAVEAPFSFRSLFG.....TRVTSFLDWIHEQMERDLKT 454
                                                                                   April 11, 2002, 08:53:27; Search time 13.3 Seconds (without alignments) 1251.566 Million cell updates/sec
                                                     US-09-846-512-12
                                                                                                                                                                                                                   GenCore version
Copyright (c) 1993 - 2000
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Compugen Ltd
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BLOSUM62 Gapop 10.0 , 100059 seqs, 36664827 residues Gapext 0.5

Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum Maximum DB DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	21	Result No.
864.5 704 661.5 660.5 660.5 650 657 657 550 550 550 550 550 550 550 550 550 5	244	Score
22222222222222222222222222222222222222		Query Match I
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HUMA HUMA HUMA HUMA HOUSE HOUS	TMS3_HUMAN	ID
393 homo 393 homo 393 homo 383 homo 981 homo 981 homo 981 homo 072 bos 073 homo 074 sus 453 mus 5511 ratt 5272 rats 5262 mus 5262 mus 576 homo 576 homo 576 homo 576 homo 577 mus 576 homo 579 homo 570 mus 571 mus 572 homo 573 homo 574 homo 575 homo 576 mus 577 mus 577 mus 578 homo 579 homo 579 homo 570 mus 571 mus 572 mus 573 mus 574 homo 575 homo	P57727 homo sapien	

Recessive deafness.";
Nat. Genet. 27:59-63 (2001).

Nat. Genet. 27:59-63 (2001).

I Genet. 27:59-63 (2001).

I SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).

I ALTERNATIVE PRODUCTS: 4 ISOFORMS; A (SHOWN HERE), B/C, D AND TRUNCATED/TAGS-12Y, ARE PRODUCED BY ALTERNATIVE SPICING.

I TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES. THE TRUNCATED ISOFORM IS FOUND AT INCREASED LEVELS IN SOME CARCINOMAS.

I SOFORM IS FOUND AT INCREASED LEVELS IN SOME CARCINOMAS.

I DISEASE: DEFECTS IN TMPRESS ARE A CAUSE OF TWO FORMS OF AUTOSOMAL NEUROSENSORY CHILDHOOD-ONSET FORMS OF DEAFNESS, DENB8 AND DFNB10.

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its content is in no way useful and the content is in no way useful.

SIMILARITY: CONTAINS 1 SRCR DOMAIN.
SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.

TRYPSIN FAMILY

ALIGNMENTS

	recessive deafiness ".	
	protesse causing both congenital and childhood onset any morning	
	**Insertion of heta-satellite repeats identifies a transmembrane	
	Rossier C., Korostishevsky M., Gal A., Shimizu N., Bonne-Tamir B.,	
_	Younus F., Mehdi S.Q., Radhakrishna U., Papasavvas M.P., Gehrig C.,	
_	Guipponi M., Wang J., Kawasaki K., Asakawa S., Minoshima S.,	
_	Scott H.S., Kudoh J., Wattenhofer M., Shibuya K., Berry A., Chrast R.,	
2	MEDLINE=20578749; PubMed=11137999;	
.	UENCE FROM N.A. (ISOFORMS A; B/C AND D), AND VARIANT	
•		
<u>ક</u>	Biochim. Biophys. Acta 1502:337-350(2000).	_
_	"Ovarian tumor ceits express a nover muiti-domain ceit surrace serine	
	Wang Y., Parmley T.H., O'Brien T.J.;	
•	Underwood L.J., Shigemasa K., Tanimoto H., Beard J.B., Schneider E.N.,	-
	MEDLINE=20521358; PubMed=11068177;	
	TISSUE=Ovarian carcinoma;	
	SEQUENCE FROM N.A. (ISOFORMS A AND TRUNCATED).	-
	[1]	_
	NCBI_TaxID=9606;	
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens (Human).	
	TMPRSS3 OR TADG12 OR ECHOS1.	_
	TADG-12) (TUMOR ASSOCIATED DIFFERENTIALLY-EXPRESSED GENE-12 PROTEIN).	
	TRANSMEMBRANE PROTEASE, SERINE 3 (EC 3.4.21) (SERINE PROTEASE	•
	20-AUG-2001 (Rel. 40, Last annotation update)	
	20-AUG-2001 (Rel. 40, Last sequence update)	-
	20-AUG-2001 (Rel. 40, Created)	-
	P57727;	
	TMS3_HUMAN STANDARD; PRT; 454 AA.	_
	IS3_HUMAN	S 6
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Query Match
Best Local Sim
Matches 454;
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Pfan; PF00530; SRCR; 1.

Pfan; PF00089; trypsin; 1.

SMART; SM00192; LDLa; 1.

SMART; SM00202; SR; 1.

SMART; SM00202; Tryp_SPC; 1.

PROSITE; PS001209; LDLRA_2; 1.

PROSITE; PS00420; SRCR_1; FALSE_NEG.

PROSITE; PS00420; SRCR_2; 1.

PROSITE; PS00420; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
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InterPro;
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AB038157;
AB038158;
AB038159;
AB038160;
605511;
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605316;
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rPro; IPR002172; 
rPro; IPR001190; 
rPro; IPR001254; 
rPro; IPR001254; 
pF00057; Idl_re
                           Similarity
      100.
nilarity 100.
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BAB20077.
BAB20078.
BAB20079.
BAB20080.
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                                                                                                        MW;
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SRCR.

SERINE PROTEASE.

CHARGE RELAY SYSTEM (BY SIMILARITY).
CLEAVAGE (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY
                                                                                                                                                            MISSING (IN TRUNCATED ISOFORM
V -> I.
/FTId=VAR_010781.
LKEFFPIIVI -> FEVFSQSSSL (IN R
A -> T (IN REF. 1).
MISSING (IN REF. 1).
ICHRDVYGGISESMLCAGYLTGGVD -
        0
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SIGNAL-ANCHOR
(POTENTIAL).
                                                                                                    HHLPLHALRGLPDGWRWN (IN REF. E -> D (IN REF. 1).; 57ECC3678F7D6AFF CRC64;
      Score 2447;
Pred. No. 6.9
); Mismatches
                                                                                                                                                                                                                                                                                                                             DLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYH
PRERADRRGRKLLCWRKPTKMKGPRPSHS (IN
                                                                                                                                                                                                                                                                                                              TRUNCATED
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                                                                                                                                                                                                                                                                                       ISOFORM).
IN TRUNCATED
DB 1;
3.9e-201;
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OR (TYPE-II
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      0;
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      Gaps
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RESULT 2
TMS2_MOUSE
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TMS2_MOUSE STANDARD; PRT; 490 AA. 09JI08; 09JKC4; 09QY82; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) TRANSMEMBRANE PROTEIN X).
                                                                                                Submitted [3]
                                                                                                        "Putative transmembrane
                                                                                         SEQUENCE FROM
                                                                                                                                    SEQUENCE
                                                                                                                                                                                       MEDLINE=21104370;
                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                 STRAIN-BALB/C
                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                              TMPRSS2.
                                                                                                                                                              human
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"Expression of transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                     361
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                                                                                                                                                                                                                                                   musculus
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                                                                                                                                                                                                                                                                                                                                                                           FGIGCAEVNKPGVYTRVTSFLDWIHEQMERDLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCGGSVITPLWIITAAHCYYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR
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                                                                                                                                                              tissues.";
                                                                                                                        Kim S.;
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                                                                                                                                                                                                                                                   (Mouse)
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Rodentia;
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                                                                                                         protease x.'";
the EMBL/GenBank/DDBJ
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Sciurognathi; Muridae;
                                                                                                                                                                                                         SPECIFICITY
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protease TMPRSS2 i
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IN PROSTATE
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SMART; SM00202; Tryp_SPc; 1.

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PROSITE; PS001420; SRCR_1; FALSE_NEG.

PROSITE; PS001420; SRCR_2; 1.

PROSITE; PS50287; SRCR_2; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS50134; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
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PVAPDADAVAAQILSLLPLKFFPIIV---
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IPR002172; LDL_recept_A.
IPR001190; SRCR.
IPR001254; Trypsin.
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                                                                                                                                                                                                         07D2B03EA4D8A1A9
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[2]
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MEDLINE=21104370; PubMed=11169526;
Vaarala M.H., Porvari K.S., Kellokumpu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paoloni-Giacobino A., Chen H.,
Antonarakis S.E.;
"Cloning of the TMPRSS2 gene, v
with transmembrane, LDLRA, and
Genomics 44:309-320(1997).
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15-JUL-1998 (Rel. 36, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3
                                                                     between
                                                                                                                                                                                                                                                                                                         human tissues."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. PubMed=11414763;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                             'Expression of transmembrane serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mutation
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SUBCELLULAR LOCATION: TYPE II MEMBRANE ITSSUE SPECIFICITY: EXPRESSED STRONGLY EXPRESSED IN PROSTATE, COLON, STOMACH, STIMILARITY: BELONGS TO PEPTIDASE FAMILY
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the Swiss Institute of Bioinformatics and the EMBL
pean Bioinformatics Institute. There are no restrict
non-profit institutions as long as its content is
and this statement is not removed.
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PROSITE: PS500420; SRCR_1; FALSE_NEG.

PROSITE: PS50287; SRCR_2; 1.

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PF00089; trypsin; 1
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SIGNAL-ANCHOR (TYPE-II MEMBRANE
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5; Mismatches 148;
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EMBL; AB016423; BAB20278.1; -.
EMBL; AB041037; BAB40328.1; -.
InterPro; IPR001190; SRCR.
InterPro; IPR001254; Trypsin.
InterPro; IPR001314; Chymotrypsin.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
                                   PRINTS; PRO0722: CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_EER; FALSE_NEG.
PROSITE; PS00420; SRCR_1; FALSE_NEG.
PROSITE; PS50287; SRCR_2; FALSE_NEG.
PROSITE; PS50287; SRCR_2; FALSE_NEG.
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PROSITE; PS50287; SRCR_2; Transmembrane; Signal-anchor;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TRANSMEMBRANE PROTEASE, SERINE 5 (EC 3.4.21.-)
                                                                                                                                                                                                                                                                   entities requires a license agreement or send an email to license@isb-sib o
                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning of mouse type 4 spinesin.";
Submitted (MAR-2000) to the EMBL/GenBank/DBA databases.
-!- SUBCELULIAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL):
-!- ALTERNATIVE PRODUCTS: 4 ISOFORMS: 1, 2, 3 AND 4 (SHOWN HERE);
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Mitsui S., Yamaguchi
              Glycoprotein;
DOMAIN
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                                                                                                                                                                                                          -SWTIQVGLVSLLDNPAPSH----LVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQP
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 (Human)
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, Last sequence update)
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,SE, SERINE 5 (EC 3.4.21.
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 704; DB 1;
Pred. No. 1.8e-52;
3; Mismatches 162
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SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                       PRT;
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-> G (IN REF. 1; BAB20277).
5CFC31789C6899AA CRC64;
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3.4.21.-)
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Best Local S
Matches 149
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SMART; SM00202; SR; 1.
SMART; SM00202; STyp_SPc; 1.
SMART; SM00202; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
PROSITE; PS00420; SRCR_1; FALSE_NEG.
PROSITE; PS00427; SRCR_2; FALSE_NEG.
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SEQUENCE
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DOMAIN
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"Molecular cloning of human spinesin.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001190; SRCR.
InterPro; IPR001254; Trypsin.
InterPro; IPR001314; Chymotrypsin.
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Mammalia; Eutheria;
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EEALLPALPKTVSFRINSEDFLLEAQVRDQPRWLLVCHEGWSPALGLQICWSLGHLRLTH
                                          QNAVL----
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                                                                                                                                                              al Similarity
149; Conser
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243
374
401
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218
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                                                                                                                                                                             28.
35.
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SRCR.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (I
CHARGE RELAY SYSTEM (I
CHARGE RELAY SYSTEM (I
CHARGE RELAY SYSTEM (I
CHARGE RELAY SYSTEM).
BY SIMILARITY.
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Pred. No. 8.66
8; Mismatches
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SIGNAL-ANCHOR
(POTENTIAL).
                                      QVFTAASWKTMCSDDWKGHYANVACAQLGFPSYVS
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                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                  Length 457;
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Leytus S.P., Loeb K.R., Hagen F.S., Kurachi K., Davie E.W.;
Leytus S.P., Loeb K.R., Hagen F.S., Kurachi K., Davie E.W.;
"A novel trypsin-like serine protease (hepsin) with a putative
transmembrane domain expressed by human liver and hepatoma cell
Biochemistry 27:1067-1074(1988).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                             mammalian cell growth.";
Proc. Natl. Acad. Sci. U.S.A. 90:
-!- FUNCTION: PLAYS AN ESSENTIAL
                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
MEDLINE-93348237; PubMed-8346233;
Torres-Rosado A., O'Shea K.S., Tsuji A.,
"Hepsin, a putative cell-surface serine |
                                                                                                                                                                                                                                                                                                                                                                                                             Chou S.H., Kurachi K.;

"Hepsin, a cell membrane-associated protease.
tissue distribution, and gene localization.";
J. Biol. Chem. 268:16948-16953(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91358502; PubMed=1885621; Tsuji A., Torres-Rosado A., Arai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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HPN OR TMPRSS1
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01-NOV-1997
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SIMILARITY: BELONGS
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TISSUE SPECIFICITY: PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A., Torres-Rosado A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1988 (Rel. 09, Created)
-1988 (Rel. 09, Last seq
-1997 (Rel. 35, Last ann
PROTEASE HEPSIN (EC 3.4
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                                                                                           FAMILY.
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Primates;
                                                                                                                   TO PEPTIDASE FAMILY S1;
                                                                                                                                                                 PRESENT
                                                                                                                                                                                    TYPE
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annotation
3.4.21.-) (
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                                                                                                                                                                                                                             90:7181-7187(1993).
TAL ROLE IN CELL GROWTH
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Catarrhini;
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                                                                                                                                                               MEMBRANE PROTE
N MOST TISSUES,
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                                                                                                                                                                                                                                                                                                                              Chou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae;
                                                                                                                                                                                    PROTEIN
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                                                                                                                                                                                                                                                                                                   Kurachi K.
required
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Best Local Similarity
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Interpro; IPR001190, SRCI
Interpro; IPR001254; Tryj
Interpro; IPR001254; Tryj
Pfam; PF00089; trypsin;
PRINTS; PR00722; CHYMOTR
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SEQUENCE
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SMART; SM00020; TYVP_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S00845; S00845.
HSSP; P00763; 1DPO.
MEROPS; S01.224; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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 349
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CQGDSGGPFVCEDSISRTPRWRLCGIVSWGTGCALAQKPGVYTKVSDFREWIFQAIK
              CQGDSGGPLVCQE----RRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME
                                                   ICTVTGWGNTQ-YYGQQAGVLQEARVPIISNDVCNGADFYGNQIKPKMFCAGYPEGGIDA
                                                                   L---VEKIVYHSKYKPKR-----LGNDIAĻMKLAGPLTENEMIQPVCLPNSEENFPDGK
                                                                                                                                                                    VSLRYDGAHLCGGSLLSGDWVLTAAHC--
                                                                                                                                                                                                                                         PDDKVTALHHSVYVRE-----GCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQ
                                                                                                                                                                                                                                                                                                         VF--TAASWKTMCSDDWKGHYANVACAOLGEPSYVSSDNLRVSSLEGQEREEFVSIDHLL 176
                                                                                                                                                                                                                                                                                                                                     LLLLTAIG-----AASWAIVAVLLRSD-----QEPLYPVQVSSADARLM
                                                                                                                                                                                                                                                                                                                                                               LILALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQ
                                                                                                           LQLGVQAVVYHGGYLPFRDPNSEENSNDIALVHLSSPLPLTEYIQPVCLPAAGQALVDGK
                                                                                                                                                                                            ASLQFQGYHLCGGSVITPLWIITAAHCVYDLYLPK-----SWTIQVGLVSLLDNPAPSH
                                                                                                                                                                                                                          ----GRLPHTQRLLEVISVCDCPRGRFLAAICQDCGRRKLPVDRIVGGRDTSLGRWPWQ
                                                                                                                                                                                                                                                                               VFDKTEGTWRLLCSSRSNARVAGLSCEEMGFLRALTHSELDVRTAGANGTSGFFCVDE--
                                                                                                                                                                                                                                                                                                                                                                                            149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΜW.
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SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Signal-anchor.
NON-CATALYTIC CHAIN (POTENTIAL).
CATALYTIC CHAIN (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SIGNAL ANCHOR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                        Score 664.5; I
Pred. No. 3.7e
62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                   -FPERNRVLSRWRVFAGAVA---QASPHG
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3.7e-49;
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ENTK_MOUSE STANI
AC P97435;
DT 01-NOV-1997 (Rel. 3:
DT
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-I- SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAINS.
-I- SIMILARITY: CONTAINS 2 CUB DOMAINS.
-I- SIMILARITY: CONTAINS 1 SEA DOMAIN.
-I- SIMILARITY: CONTAINS 1 SEA DOMAIN.
-I- SIMILARITY: CONTAINS 1 SEA DOMAIN.
-I- SIMILARITY: CONTAINS 1 STATEMENT SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRSS7 OR ENTE.

Mus musculus (Mouse).

Mus musculus (Mouse).

Charvota; Metazoa; Chordata; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U73378; AAB37317.1; HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure of murine enterokinase (enteropeptidase) and expression small intestine during development."; Am. J. Physiol. 274:6342-6349(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6; TISSUE=Duodenum;
MEDLINE=98147142; PubMed=9486188;
Yuan X., Zheng X., Lu D., Rubin D.C., Pung C.Y.M., Sadler J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HETERODIMER OF A CATALYI MULTIDOMAIN (HEAVY) CHAIN LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: RESPONSIBLE FOR INITIATING ACTIVATION OF PANCREATIC PROTECLYTIC PRODENZYMES (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPEPTIDASE A). IT CATALYZES THE CONVERSION OF TRYPSINOGEN TO TRYPSIN WHICH IN TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYSSINOGEN, PROCARBOXYPEPTIDASES, AND PROELASTASES (BY SIMILARITY). CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF 6-LYS-|-ILE-7 BOND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRYPSIN FAMILY.
"AM; SEA; 1.
") SECR; 1.
") SECR; 1.
") SECR; 1.
") SECR; 1.
"() SECR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; IPR000859; CUB.
; IPR001314; Chymotrypsin.
; IPR002172; LDL_recept_A.
; IPR000998; MAM.
; IPR000982; SEA.
; IPR001190; SRCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  CUB;
                                                                                                                                                                                                                                                                                                                                                                                   ld1_recept_a;
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1. 35, Last sequence update)
1. 40, Last annotation update)
(EC 3.4.21.9) (ENTEROKINASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART;
                              122
                                               682
                                                               67
TALHHSVYVREG--CASGHVVTLQCT--ACGHRR---GYSSRIVGGNMSLLSQWPWQASL 234
               HSIWHIACAENWTTQISNEVCHLLGLGS--ANSSMPISSTGG---GPFVRVNQ-----
                              AASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKV
                                               LGIPEPCQDDEFQCKDG-NCIPLGNLCDSYPHCRDGSDEASCVRFLNGTRSNNGLVQFNI 740
                                                               LGIHFDC-SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVR----VGGQNAVLQVFT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00202;
SM00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protease;
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; PS50024; SEA; 1.
; PS00420; SRCR_1; FALSE;
; PS50287; SRCR_2; 1.
; PS50287; SRCR_2; 1.
; PS50240; TRYPSIN_DOM; 1
; PS00134; TRYPSIN_HIS; 1
                                                                                      Similarity
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PS01209;
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                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zymogen;
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37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Repeat.

NON-CATALYTIC CHAIN (HEAVY CHAIN).

CATALYTIC CHAIN (LIGHT CHAIN).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
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Pred.
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N-LINKED
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CHARGE
                                                                                                                       N-LINKED (GLCNAC: W; E62549E463743C3D
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                                                                               Mismatches
                                                                                      661.5; DB
No. 2e-48;
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RELAY SYSTEM
RELAY SYSTEM
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RELAY SYS
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(GLCNAC)
(GLCNAC)
                                                                                                                                                                      GLCNAC.
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                                                                               Gaps
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TRESULTION AND THE PROPERTY OF THE PROPERTY OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         trachea, colon, and small intestine: identific chromosomal localization.";
Submitted (DEC-1990)
                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databaser: FUNCTION: MAY PLAY A ROLE IN TUMOR PROGRESSION, FORMATION AND TUMOR INVASION.

-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (
-!- TISSUE SPECIFICITY: HIGH LEVELS IN PANCREATIC, C
AND AMPULLARY CANCER, VERY WEAK EXPRESSION IN NO GASTROINTESTINAL AND UROGENITAL TRACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9NRS4: O9NZA5;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TRANSMEMBRANE PROTEASE, SERINE 4 (EC 3.4.21.-)
                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-Pancreatic carcinoma;
TISSUE-Pancreatic carcinoma;
MEDLINE-20283276; PubMed-10825129;
Wallrapp C., Haehnel S., Mueller-Fillasch
Twamura T., Ruthenbuerger M., Lerch M.M.,
                                             EMBL; AF179224; EMBL; AF216312;
                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEASE 2) (MT-SP2). TMPRSS4 OR TMPRSS3.
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                                                                                                                                                                                                                                     between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A novel transmembrane serine protease (TMPRSS3) overexpressed pancreatic cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TMS4_HUMAN
                     InterPro;
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                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 SRCR DOMAIN. SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS
                                                                                                                                                                                                                                                                                                                                                       TRYPSIN FAMILY.
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16312; AAF31436.1;
IPR001314; Chymoti
IPR002172; LDL_rec
                                                                                                                 email
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                                                                   AAF74526.1;
                                                                                                                    to license@isb-sib.ch).
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Chymotrypsin LDL_recept_A
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Adler G., Gress
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DOMAIN
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PROSITE; PS0068; LDLRA_2; FALSE_NEG
PROSITE; PS00420; SRCR_1; FALSE_NEG
PROSITE; PS00420; SRCR_2; 1.
PROSITE; PS50287; SRCR_2; 1.
PROSITE; PS00134; TRYPSIN_DM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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Pfam; PF00057; ldl_recept_a;
Pfam; PF00089; trypsin; 1.
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CNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQ
                                CNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVN
                                                                                   LAGPLIFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLNHAAVPLISNKI
                                                                                                                                                                                                                     SGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITA
                                                                                                                                                                                                                                                                                                                                  CDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALA
                                                                                                                                                                                                                                                                                                                                                                     CDGVSDCKDGEDEYRC-----
                                                                                                                                                                                                                                                                                                                                                                                                  IPMETERKVGIPIIIALLSLASIIIVVVLIKVILD---KY----YFLCGQPLHFIPRKQL
                                                                                                                                   AHCFRKHTDVF---NWKVRAGSDKL--GSFPSLAVAKIIIIEFNPMY-PK--DNDIALMK
                                                                                                                                                                 AHCV---YDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIV---YHSKYKPKRLGNDIALMK
                                                                                                                                                                                                  SGSLVSLHCLACG-KSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA
                                                                                                                                                                                                                                                                    ETACROMGYSS - -
                                                                                                                                                                                                                                                                                                 NVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHHSVYVREG--
                                                                 LQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00192; LDLa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SR; 1.
Tryp_SPc;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protease;
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437
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2290
387
205
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92
1183
310
246
410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARGE RELAY SYSTEM (BY SIMILARITY CHARGE RELAY SYSTEM (BY SIMILARITY CHARGE (POTENTIAL).

BY SIMILARITY.

BY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                                  KPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL-ANCHOR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDL-RECEPTOR CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                   -VRVGGQNAVLQVFTAA--SWKTMCSDDWKGHYA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; DB 1;
3.6e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e; Signal-anchor (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Þ
   WHYVGIVSWGYGCGGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Y SIMILARITY).
Y SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
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                                                                                                                                                                                                                                                                                               -CA
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Q

430

452

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RESULT 9
ENTE_BOVE
ID FERB
DT 01-FERB
OC MCBLIT
RN KILAMC
RT FERCE
RT FOOC.
RN [1]
RN FERCE
RT FOOC.
RN [2]
RP SEQUEN
RY EDLIN
RA LLAVALI
RA FERCE
TISSUE
RT FOOC.
RT SEQUEN
RC 11-SUM
RC 11
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p98072;
01-FEB-1996 (Rel. 33, Creat
01-FEB-1996 (Rel. 33, Last
20-AUG-2001 (Rel. 40, Last
ENTEROPEPTIDASE PRECURSOR (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 801-1035 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-94043122; PubMed-8226855;
Lavallie E.R., Rehemtulla A., Racie L.A., Diblasio E.A.,
Ferenz C., Grant K.L., Light A., McCoy J.M.;
"Cloning and functional expression of a cDNA encoding the catalytic subunit of bovine enterokinase.";
J. Biol. Chem. 268:23311-23317(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Intestine;
MEDLINE=92189715; PubMed=1799406;
              entities requires
or send an email 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enterokinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kitamoto Y., Yuan X., Wu Q., McCourt D.W., Sadler J.E.; "Enterokinase, the initiator of intestinal digestion, is protease composed of a distinctive assortment of domains. Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994).
                                                                                                                                                                                                                                                                                        TRYPSINOGEN.

TRYPSINOGEN.

SUBUNIT: HETERODIMER OF A CATALYTIC (LIGHT) CHAIN MULTIDOMAIN (HEAVY) CHAIN LINKED BY A DISULFIDE BC SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PF 1- TISSUE SPECIFICITY: INTESTINAL BRUSH HORDER.

THE CHAINS ARE DERIVED FROM A SINGLE PRECURSO CLEAVED BY A TRYPSIN-LIKE PROTEASE.

CLEAVED BY A TRYPSIN-LIKE PROTEASE.

SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAIN.

SIMILARITY: CONTAINS 2 CUB DOMAIN.

SIMILARITY: CONTAINS 1 SEA DOMAIN.

SIMILARITY: CONTAINS 1 SECR DOMAIN.

SIMILARITY: CONTAINS 1 SECR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Protein Chem. 10:475-480(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The amino-terminal sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Light A., Janska H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 801-827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94329561; PubMed=8052624; Kitamoto Y., Yuan X., Wu Q., McCo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Duodenum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415
                         s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is ified and this statement is not removed. Usage by and fo ities requires a license agreement (See http://www.isb-sib.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: RESPONSIBLE FOR INITIATING ACTIVATION OF PANCREATIC PROTECTIVE PROTECTIONS: (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPEPTIDASE A). IT CATALYZES THE CONVERSION OF TRYPSINGGEN TO TRYPSIN WHICH IN TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSINGGEN, PROCARBOXYPEPTIDASES, AND PROELASTASES.

CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF 6-LYS-1-ILE-7 BOND IN
                                                                                                                                                                                                                                                     TRYPSIN FAMILY
                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPGVYTKVSAYLNWIYNVWKAEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OR ENTK
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Last sequence update)
Last annotation update)
RSOR (EC 3.4.21.9) (ENTEROKINASE).
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                                                                                                                                                                                                                                                                         MAM DOMAIN.
PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         437
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                                                                                                                                                                                                                                                                            ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                            KNOWN
                                                                                                                                   restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND
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                                                                                                                                                                  a collaboration -
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Pfam; PF00Uby; CLIFMOTRYPSIN.
PRINTS; PR00722; CHE; 2.
SMART; SM00192; LDLa; 2.
SMART; SM00192; LDLa; 2.
SMART; SM00137; MAM; 1.
R SMART; SM00200; SEA; 1.
R SMART; SM00200; SF; 1.
R SMART; SM00200; Tryp_SPC; 1.
SMART; SM00020; Tryp_SPC; 1.
                                                                                                                                                  LIPID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U09859; AAB4002
EMBL; L19663; AAA1603
PIR; A61436; A61436.
HSSP; P00763; 1DPO.
                               CARBOHYD
CARBOHYD
                                                               CARBOHYD
CARBOHYD
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ACT_SITE
ACT_SITE
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DOMAIN
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PROSITE;
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                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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InterPro;
                                                                                                         CARBOHYD
                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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MEROPS; S01.156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
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E; P$50068; LL.

TE; P$50060; MAM_1; _

JITE; P$50060; MAM_2; 1.

JSITE; P$50024; SEA; 1.

OSITE; P$50024; SRCR_1; FALSE_NEG.

"TIE; P$50240; TRYPSIN_HIS; 1.

"RYPSIN_HIS; 1.

"RYPSIN_SER; 1.

"RYPSIN_SER; 1.

"RYPSIN_SER; 1.

"RYPSIN_SER; 1.
"RYPSIN_SER; 1.
"RYPSIN_SER; 1."
"SIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; PF00431; CUB; 2.
1; PF00057; Idl_recept_a; 1, 1; PF00629; MAM; 1.
1; PF01390; SEA; 1.
1; PF00530; SRCR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J IPRO01859; CUB.
J IPRO01314; Chymotrypsin.
J IPR002172; LDL recept_A.
J IPR000998; MAM.
J IPR001099; SEA.
J IPR001199; SECR.
J IPR0011254; Trypsin.
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AAA16035.1;
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CATALYTIC CHAIN (LIGHT CHAIN).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
SEA.
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                                                                                                                                                                                                                                                                                                   SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
MYRISTATE (POTENTIAL).
 BY SIMILARITY.
N-LINKED (GLCNAC
N-LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ν
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CUB 1.
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 GLCNAC.
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                                                                                                                                                                                                SIMILARITY).
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(BY)
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Dagand Bloecker

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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seq
20-AUG-2001 (Rel. 40, Last ann
                                                                            TISSUE=Duodenum;

MEDLINE=95234679; PubMed=7718557;

Kitamoto Y., Veile R.A., Donis-Keller H., So

"cDNA sequence and chromosomal localization
the proteolytic activator of trypsinogen.";

Biochemistry 34:4562-4568(1995).
     Holzinger
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLGIPEPCKEDNFQCKDG-ECIPLVNLCDGFPHCKDGSDEAHCVRLFNGTTDSSGLVQFR
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AR Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
AR Hattori M., Fujiyama A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
AR All Hattori M., Fujiyama A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
AR All Hattori M., Totokai Y., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
AR All Hattori M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley
AR Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
AR Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
AR Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
AR Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.
AR Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.
AR Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
AR Minoshima S., Schen O., Desario A., Reichelt J., Kauer G., Bloecker
AR Amser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.
AR Mehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
AR Lehrach H., Reinhardt R., Yaspo M.-L.;

"The DNA sequence of human chromosome 21.";

Nature 405:311-319(2000).
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Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994).

-i- FUNCTION: RESPONSTBLE FOR INITIATING ACTIVATION OF PANCREATIC PROTEOLYTIC PROENZYMES (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPEPTIDASE A). IT CATALYZES THE CONVERSION OF TRYPSINOGEN TO TRYPSIN WHICH IN TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSINOGEN, PROCARBOXYPEPTIDASES, AND PROENZYMES INCLUDING CHYMOTRYPSINOGEN, PROCARBOXYPEPTIDASES, AND PROENZYMES OF 6-LYS-1-ILE-7 BOND IN TRYPSINOGEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HETERODIMER OF A CATALYTIC (LIGHT) CHAIN AND A MULTIDOMAIN (HEAVY) CHAIN LINKED BY A DISULFIDE BOND. SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE). TISSUE SPECIFICITY: INTESTINAL BRUSH BORDER. THAT IS THE CHAINS ARE DERIVED FRAME A SINGLE PRECURSOR THAT IS CLEAVED BY A TRYPSIN LIKE PROTEASE.

DISEASE: DEFECTS IN PRSS7 CAUSE LIFE-THREATENING INTESTINAL DISEASE:
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7 009860 AAC50138.1

7 19124 CAB65555.1

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SMARR; SM00193; MAM; 1.
SMARR; SM00200; SEA; 1.
SMARR; SM00200; Tryp_SPC; 1
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SMARR; SM00200; Tryp_SPC; 1
PROSITE; PS01180; CUB; 2.
PROSITE; PS0109; LDLRA_1; PROSITE; PS00060; MAM_1; 1.
PROSITE; PS50060; MAM_2; 1.
PROSITE; PS500740; MAM_2; 1.
PROSITE; PS500740; SECR_1; F
PROSITE; PS500740; SECR_1; F
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PROSITE; PS500740; SECR_1; F
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PROSITE; PS500740; TRYPSIN_B
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InterPro;
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MIM; 226200;
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erPro; IPR002172; LDL_recept_A.
erPro; IPR002172; LDL_recept_A.
erPro; IPR000998; MAM.
erPro; IPR000998; SEA.
erPro; IPR001190; SRCR.
erPro; IPR001254; Trypsin.
erPro; IPR001254; Trypsin.
m; PF00431; CUB; 2.
m; PF00457; ldl_recept_a; 2.
m; PF00629; MAM; 1.
m; PF00530; SEA; 1.
m; PF00530; SRCR; 1.
m; PF00889; trypsin; 1.
m; PF00889; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X19137; CAB65555.1; J

X19138; CAB65555.1; J

X19139; CAB65555.1; J

X19140; CAB65555.1; J

X19141; CAB65555.1; J

X19142; CAB65555.1; J

X19143; CAB65555.1; J

X19143; CAB65555.1; J

X19143; CAB65555.1; J

X19143; CAB65555.1; J

X1163218; CAB90332.1; AL163217; CAB90389.1; P00763; LDPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protease;
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trypsin; 1.
2; CHYMOTRYPSIN.
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SRCR_1; FALSE_NEG.
SRCR_2; 1.
TRYPSIN_DOM; 1.
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LDLRA_2; 2.
LDLRA_2; 1.
MAM_1; 1.
MAM_2; 1.
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223
334
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CUB 2.

CUB 2.

CUB 2.

CUB 2.

CUL-RECEPTOR CLASS A 2.

SERINE PROTEASE.

SERINE PROTEASE.

CHARGE RELAY SYSTEM (BY CHARGE RELAY SYSTEM (BY CHARGE RELAY SYSTEM (BY SIMILARITY.

BY SIMILARITY.
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LDL-RECEPTOR
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NON-CATALYTIC CHAIN (HEAVY CHAIN).
CATALYTIC CHAIN (LIGHT CHAIN).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
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                                                                  Sus scrofa (Pig).
Eukaryota; Metazoa; (Mammalia; Eutheria; (MCBI_TaxID=9823;
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CARBOHYD
 SEQUENCE FROM N.A., ANI
TISSUE=Duodenal mucosa
MEDLINE=94327548; PubMo
                                                                                                                                         ENTK_PIG STANDARD; PRT; 1034 AA.
p98074;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ENTEROPEPTIDASE PRECURSOR (EC 3.4.21.9) (ENTEROKINASE)
PRSS7 OR ENTK
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Cetartiodactyla; Suina;
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37.7%;
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N-LINKED (GL
                                   PARTIAL SEQUENCE
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Pred. No. 4.6e
57; Mismatches
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No. 4
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ina; Suidae;
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.6e-48;
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(POTENTIAL).
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(POTENTIAL).
                                                                                         SuS
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-TVVYQGT

923

352

864

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236

292

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Gaps

15;

121

181 695

747

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JEE; PS0110.

JIE; PS0110.

JIE; PS0110.

JIE; PS00108; LDLRA_,

JSITE; PS50068; LDLRA_,

JSITE; PS500740; MAM_1; 1.

ACSITE; PS500740; MAM_2; 1.

PROSITE; PS50024; SER, 1.

PROSITE; PS50024; SER, 1.

PROSITE; PS50027; SRCR_1; FALSE_NEG.

PROSITE; PS500240; TRYPSIN_DOM; 1.

PROSITE; PS50014; TRYPSIN_HIS; 1.

DR PROSITE; PS000135; TRYPSIN_SER; 1.

DR PROSITE; PS000135; TRYPSIN_SER; 1.

Seine protease; Zymogen; Transmembrane; P

Seine protease; Zymogen; Transmembrane; P

TN S1118 799 NON-CATALYTI

118 799 NON-CATALYTI

ACTALYTIC
                                                       InterPro; IPR00
Pfam; PF00431;
Pfam; PF00057;
Pfam; PF00629;
Pfam; PF01390;
Pfam; PF00530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-orsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                SMART; SP
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miki K., Kurokawa K., Tashiro K., Shiokawa K., Shinomiya K.,
Umeyama H., Inoue H., Takahashi T., Takahashi K.;
Umeyama H., Inoue H., Takahashi T., Takahashi K.;
"Structural characterization of porcine enteropeptidase.";
J. Biol. Chem. 269:19976-19982(1994).

-i- FUNCTION: RESPONSIBLE FOR INITIATING ACTIVATION OF PANCREATIC
PROFECTIVES THE CONVERSION, CHYMOTRYPSIN AND CARBOXYPEPTIDASE
A). IT CATALYZES THE CONVERSION OF TRYESINGEN TO TRYESIN WHICH IN
TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSINOGEN,
PROCARBOXYPEPTIDASES, AND PROELASTASES.
-I- CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF 6-LYS-|-ILE-7 BOND IN
TRYESINGEN.
-I- CATALYTIC HETEROTRIMER OF A CATALYTIC (LIGHT) CHAIN, A MULTIDOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsushima
Miki K., Ku
Umeyama H.,
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECUI
CLEAVED BY A TRYPSIN-LIKE PROTEASE.
-!- PTM: THE MINI CHAIN MAY BE CLEAVED BY ELASTASE.
-!- SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOM-
-!- SIMILARITY: CONTAINS 2 CUB DOMAIN.
-!- SIMILARITY: CONTAINS 1 SEA DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HEAVY) CHAIN, AND A MINI CHAIN. SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                             IS: PR00722; CHYMOTRYPSIN
[; SM00042; CUB; 2.
[r; SM00137; MAM; 1.
[r; SM00200; SEA; 1.
[r; SM00200; SEA; 1.
[r; SM00200; Tryp_SPC; 1.
[r; SM00020; Tryp_SPC; 1.
[r] SM00020; Tryp_SPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                              PF00089;
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o; IPR001314; Chymotrypsin.
o; IPR002172; LDL_recept_A.
o; IPR0010998; MAM.
o; IPR001099; SEA.
o; IPR0011254; Trypsin.
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SEA;
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2; CHYMOTRYPSIN.
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                                                     Transmembrane; Repeat.
NON-CATALYTIC M CHAIN (MINI CHAIN).
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CATALYTIC L CHAIN (LIGHT CHAIN).
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Lro K., Shiokawa K., Shinomiya
nashi T., Takahashi K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                    Hydrolase;
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035453;
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Vu T.-K.H., Liu R.W., Haaksma C., Tomasek J.J., Howard I
"Identification and cloning of the membrane -associated a
protease, hepsin, from mouse preimplantation embryos.";
J. Biol. Chem. 272:31315-31320(1997).
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Pfam; PF00089;
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SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; AL:
TRYPSIN FAMILY.
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SEQUENCE
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PIR; S
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between
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proteinase.";
Biochim. Biophys. Acta
FUNCTION: PLAYS AN
                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
Mammalia; I
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; $33777; $33777.
P; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                              TRYPSIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGGPLVCQE----RRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME
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B-1994 (Rel. 28, La
V-1997 (Rel. 35, La
E PROTEASE HEPSIN (
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HEPSIN (EC 3.4
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AN ESSENTIAL ROLE IN CELL
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on update)
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InterPro; InterPro;

IPR0011314; Chymotrypsin. IPR001190; SRCR.

InterPro;

IPR001254;

Trypsin.

trypsin;

CHYMOTRYPSIN

MEDLINE=91129236; SEQUENCE FROM N.A.

kallikrein.";

G

Chretien

<u>.</u>

TER ITS BINDING BRADYKININ FROM

Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Craniața; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

PRINTS; PR00722; Pfam; PF00089;

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CARBOHYD

SEQUENCE

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Query Match
Best Local Similarity
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01-JAN-1990 (Rel. 1
01-JAN-1990 (Rel. 1
20-AUG-2001 (Rel. 4
PLASMA KALLIKREIN E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00202; SR; 1.
SMART; SM000202; Tryp_SPc; 1.
SROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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norvegicus
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40, Last and PRECURSOR
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annotation update)
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SERINE PROTEASE.

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BY SIMILARITY.

BY SIMILARITY.
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NON-CATALYTIC CHAIN (POTENTIAL).
CATALYTIC CHAIN (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 645; DB Pred. No. 1.7e il; Mismatches
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                                                                                                                       PRT;
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..7e-47;
nes 156;
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                                            (PLASMA PREKALLIKREIN)
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 InterPro; irrocal.

Pfam; pF00024; pAN; 4.

R pfam; pF00024; trypsin; 1.

R pRINTS; pR00005; APPLEDOMAIN.

R PRINTS; pR00005; APPLEDOMAIN.

R PRINTS; pR00722; CHYMOTRYPSIN.

R SMART; SM00223; APPLE; 4

)R SMART; SM0020; Tryp_SPC; 1.

JR PROSITE; PS00495; APPLE; 4

)R PROSITE; PS00495; APPLE; 4

DR PROSITE; PS00134; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW Hydrolase; Serine protease; Glycoprotein; Plasma; Zymogen;

KW Hydrolase; Serine protease; Glycoprotein; Plasma; Zymogen;

KW Hydrolase; Serine protease; Glycoprotein; Plasma; Zymogen;
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DNA 8:553-574(1989).

THE ENZYME CLEAVES LYSTARG AND ARG-SER BONDS. IT ACTIVATES, IN A RECIPROCAL REACTION, FACTOR XII AFTER ITS BINDING ACTIVATES, IN A RECIPROCAL REACTION, FACTOR XII AFTER ITS BINDING TO A NEGATIVELY CHARGED SURFACE. IT ALSO RELEASES BRADYKININ FROM HAW KININOGEN AND MAY ALSO PLAY A ROLE IN THE RENIN-ANGIOTENSIN SYSTEM BY CONVETTING PRORENIN INTO RENILS.

TSUBUNIT: THE ZYMOGEN IS ACTIVATED BY FACTOR XIIA, WHICH CLEAVES THE MOLECULE INTO A LIGHT CHAIN, WHICH CONTAINS THE ACTIVE SITE, AND A HEAVY CHAIN, WHICH ASSOCIAVES WITH HAW KININOGEN. THESE CHAINS ARE LINKED BY ONE OR MORE DISCIPLED BONDS.

TSUBLILARITY: CONTAINS 4 APPLE DOMAINS.

TRYPSIN FAMILY. PLASMA KALLIKREIN SUBFAMILY SI; ALSO KNOWN AS THE TRYPSIN FAMILY. PLASMA KALLIKREIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                 EMBL;
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MEDLINE-90091743; PubMed-2598771;
Seidah N.G., Ladenheim R., Mbikay M., Hamelin J
Rougeon F., Lazure C., Chretien M.;
"The CDNA Structure of rat plasma kallikrein.";
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                          HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement or send an email to license@isb-sib.c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long a modified and this statement is not removed.
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Seidah N.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Gene structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restructy pron-profit institutions as long as its content
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M62348; AAA74563.1;
M62347; AAA74563.1;
M62347; AAA74563.1;
M62349; AAA74563.1;
M62350; AAA74563.1;
M62351; AAA74563.1;
M62352; AAA74563.1;
M62353; AAA74563.1;
M62353; AAA74563.1;
M62354; AAA74563.1;
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                                                                                                                                                                                                                                                                                     P00750;
                                                                                                                                                                                                                                                                                                                   M58590;
                                                                                                                                                                                                                                                                                                                                     M30282;
                                                                                                                                                                                                           ; IPR000177; ; IPR001314; ; IPR003014; ; IPR001254;
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AAA42069.
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AAA74563.1;
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nski-Chupin I.,
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 19
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                                            Plasma; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
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DT 01-MA
DT 20-AU
DE PLASH
DE PLASH
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OC EUKAI
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Best Local Similarity
Matches 116; Conser
                                                                          KAL_MOUSE STAN
P26262;
01-MAY-1992 (Rel. 2
01-MAY-1992 (Rel. 2
20-AUG-2001 (Rel. 4
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DASTLEID
DISULFID
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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KLK3 OR PK.
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                                                           (FLETCHER
                                                                                                                                                                         STANDARD;
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22, Last sequence update)
40, Last annotation update)
| PRECURSOR (EC 3.4.21.34) (PLASMA PREKALLIKREIN)
LETCHER FACTOR).
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CHARGE RELAY SYSTEM.

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BY SIMILARITY.

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PLASMA KALLIKREIN LIGHT C
APPLE 1.
APPLE 2.
APPLE 3.
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Pred. No. 6.8e
52; Mismatches
                                                                                                                                                                       PRT;
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.8e-41;
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       Euteleostomi;
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       HSSP; P00750; 1RTF:

MEROPS; S01.212; ...

MGD; MGI:102849; Klk3.

MGD; MGI:102849; Klk3.

InterPro; IPR000177; Apple.
InterPro; IPR0001314; Chymotrypsin.
InterPro; IPR001314; Trypsin.
InterPro; IPR001254; Trypsin.
InterPro; IPR001254; Trypsin.
InterPro; IPR001254; Trypsin.
InterPro; P00005; APPLEDOMAIN.
Pfam; PF00005; APPLEDOMAIN.
PRINTS; PR00702; CHYMOTRYPSIN.
SMART; SM00223; APPLE; 4.
SMART; SM00223; APPLE; 4.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00495; APPLE; 4.
PROSITE; PS00495; APPLE; 4.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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Seidah N.G., Sawyer N., Hamelin J., Mion P., Beaubien G.,
Serchpapa L., Rochemont J., Mikay M., Chretien M.;
"Mouse plasma kallikrein: cDNA structure, enzyme characterization,
and comparison of protein and mRNA levels among species.";
DNA Cell Biol. 9:737-748(1990),
-!- FUNCTION: THE ENZYME CLEAVES LYS-ARG AND ARG-SER BONDS. IT
ACTIVATES, IN A RECIPROCAL REACTION, FACTOR XII AFTER ITS BINDING
TO A NEGATIVELY CHARGED SURFACE. IT ALSO RELEASES BRADYKININ FROM
HWW KININGEN AND MAY ALSO PLAY A ROLE IN THE RENIN-ANGIOTENSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M58588; AAA63393.1;
PIR; A36557; KQMSPL.
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NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                         Fibrinolysis;
                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM BY CONVERTING PRORENIN INTO RENIN.
SUBUNIT: THE ZYMOGEN IS ACTIVATED BY FACTOR XIIA, WHICH CLEAVES
THE MOLECULE INTO A LIGHT CHAIN, WHICH CONTAINS THE ACTIVE SITE,
AND A HEAVY CHAIN, WHICH ASSOCIATES WITH HMW KININGGEN. THESE
CHAINS ARE LINKED BY ONE OF MORE DISOLFIDE BONDS.
SIMILARITY: CONTAINS 4 APPLE DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY. PLASMA KALLIKREIN SUBBRAMILY.
                                                                                                                                                                                                                                                                                                                                                                                              Serine
   Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
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PLASMA KALLIKREIN HEA
PLASMA KALLIKREIN LIG
APPLE 1.
APPLE 2.
APPLE 3.
APPLE 3.
APPLE 4.
SERINE PROTEASE.
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N-LINKED (GLCNAC...
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CHARGE RELAY SYSTEM.
BY SIMILARITY.
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tion; Inflammatory response; Liver;
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71368 MW;
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Search completed: April 11, 2002, 08:57:04 Job time: 217 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                  and is
                                                                                                                                                                                                                                                                                                                                                        Pred. No.
2432.5
2430.5
24718
2375
1788
1354
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876.5
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seq
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length: 2000000000
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Match
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1: /SIDS8/gcgdata
2: /SIDS8/gcgdata
3: /SIDS8/gcgdata
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2447
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Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                 /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:
/SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:
/SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:
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/SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:
/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:
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 AAB32246
AAY72093
AAB32247
AAB43572
AAG73966
AAY92050
AAM01315
AAY77726
                                                                                                                                               AAE06935
AAB44250
AAY41694
                                                                                                                                                                                                                                                                                  SUMMARIES
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1344.633 Million cell updates/sec
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                 Human cancer assoc
Human colon cancer
HrPCa6/7 polypepti
P1000C amino acid
                                                                                                                                                                                                                        Description
                                                                                                                                           Human membrane-typ
Human PRO382 (UNQ3
Human PRO382 prote
                                                                                          Human serine prote Tumour associated
                                                                                                                              Tumour associated
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564.5	576	583.5	600.5	646	648.5	652	652	652	655.5		656	657	657.5	660	660.5	660.5	661		6	686.5	696	702	704	704	727	731	731	864.5	864.5	864.5	864.5	868.5	875.5
	23.	23.	24.	26.	26.	26.	26.		26.	26.	26.	26.	ა	7.	27.0	27.0	7.	27.2	7.	8	28.4	8	28.8	8	9	9.	9.	5	<u>ب</u>	ر.	5	35.5	5
418	256	317	238	172	437	432	432	432	416	416	311	1019	492	798	435	435	273	417	423	283	457	414	480	445	889	562	421	492	492	492	492	393	492
17	22	22	21	22	22	22	22	21	20	20	21	22	22	15	22	20	21	22	22	21	21	21	21	21	22	22	22	22	22	21	21	22	21
AAR89435	AAB98501	AAM25633	AAB11695	AAM25245	AAE06931	AAB66166	AAB87581	AAY99417	AAW96812	AAY43325	AAB11697	AAE06940	AAY72559	AAR57283	AAY72558	AAY06437	AAB11696	AAE06942	AAE06944	AAY81492	AAB11699	AAB08912	AAB08950	AAB11698	AAE01944	AAE01943	AAB85042	AAM01294	AAE06943	AAY57280	AAB36901	AAM01317	AAY44406
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	hepsin s		Mouse serine prote			in of the i	•		se serin	hepsin	serine prot	Human enterokinase	S	Bovine enterokinas	Human seripancrin	S	Mouse serine prote	Human hepsin prote	Human transmembran										S		TMPRSS2 p	C partia	Human 20P1F12-GTC2

ALIGNMENTS

AAE06935

AAE06935 standard; Protein; 453

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AAE06935;

16-OCT-2001 (first entry)

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WO200157194-A2
                                Cleavage-site
Domain
                    Misc-difference
                                                                         Domain
                                                                                              Domain
                                                                                                                 Key
                                                     Domain
                                                                                                          Domain
                                                                                                                              Homo sapiens
                    /label=
324
                                 /note= "Trypsin-like serine protease domain"
216..217
217..443
                                                     /label= SR_domain
/note= "Scavenger receptor Cys-rich domain"
216..443
                                                                       /label= LDLRa_domain
/note= "LDL receptor
109..205
            /note= "Unpaired cysteine"
                                                                                                   /label= Transmembrane_domain
                                                                                                                Location/Qualifiers
                          Protease_domain
                                                                               domain class
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Human; transmembrane serine protease; membrane-type serine protease; MTSP; protease domain; neoplastic disease; tumour; cancer; cytostatic; lung carcinoma; colon adenocarcinoma; ovarian carcinoma; gene therapy.

Human membrane-type serine protease (MTSP) 6.

tumour supp

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γQ
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Best Local :
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18-FEB-2000;
22-JUN-2000;
26-JUL-2000;
08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to transmembrane serine proteases and their corresponding nuclectides and the protease domain of a type-II membrane-type serine protease (MTSP) mTSP is useful for identifying compounds that modulate or inhibits its proteolytic activity and for formulating a medicament for treating neoplastic disease. MTSP and its corresponding nucleotides are useful in preventing or treating tumours or cancers such as lung carcinoma, colon adenocarcinoma and ovarian carcinoma, in diagnostics and in hybridisation assays. MTSP is useful as a diagnostic marker for tumour development, growth and/or progression and as immunogens to generate antibodies that specifically bind to it. MTSP DNA is useful in a yeast two-hybrid system and in
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel single chain polypeptide comprising protease domain membrane-type serine protease or its catalytically active useful for treating and preventing cancer and tumor -
                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy. The present sequence is human MTSP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                                                                                                                                              1 MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALI
LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLNHA
                                                                                                             LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR
                                                                                                                                               vtalhhsvyvregcasghvvtlqctacghrrgyssrivggnmsllsqwpwqaslqfqgyh
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                                                  lgndialmklagpltfnemiqpvclpnseenfpdgkvcwtsgwgatedg-gdaspvlnha
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2000US-0183542.
2000US-0213124.
2000US-0220970.
2000US-0657986.
2000US-0234840.
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99.8%;
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Pred. No. 4.1e-187;
                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
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e portion
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  419
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AAC78458 to AAC78599 represent polypucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide segments.
                                                                                                                                                                                                                                                                                                                                                    29-OCT-1999
30-NCV-1999
02-DEC-1999
10-DEC-1999
16-DEC-1999
30-DEC-1999
30-DEC-1999
30-DEC-1999
05-JAN-2000
06-JAN-2000
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21-APR-1999;
28-APR-1999;
14-MAY-1999;
                                                                                                                                                                                                                      WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                               Ferrara
Goddard
                                                                                                                                                 Claim 12; Fig
                                                                                                                                                                       Novel PRO polypeptides and polynucleotides used in to target bioactive molecules to specific cells, ar cellular activities -
                                                                                                                                                                                                                                                          Shelton
                                                                                                                                                                                                                                                                     Kljavin
                                                                                                                                                                                                                                                                                                       Ashkenazi
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26-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed
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DB; AAC78475.
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sed sequence tag; detection; cancer.
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N, Filvaroff E,
A, Godowski PJ,
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99US-0142506
99WO-US28313
99WO-US28551
99WO-US38565
99WO-US31095
99WO-US31243
99WO-US31274
2000WO-US00277
2000WO-US00277
                                                                                                                                                                                                                                                          Kuo SS,
Stewart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US04341
                                                                                                                                               28; 636pp; English.
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99US-0130232.
99US-0131445.
99US-0134287.
99US-0141037.
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99US-0123957
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TA, Tumas D,
                                                                                                                                                                                                                                                         Botstein D, Desnoyers L, Eaton DL; Fong S, Gao W, Gerber H, Geritsen Grimaldi CJ, Gurney AL, Hillan KJ; ier MA, Pan J, Paoni NF, Roy MA; Tumas D, Williams PM, Wood WI;
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RESULT
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AX Huma
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Best Local Similarity 99.6%;
Matches 452; Conservative
   10 MAR-1998;
11-MAR-1998;
11-MAR-1998;
11-MAR-1998;
12-MAR-1998;
13-MAR-1998;
17-MAR-1998;
20-MAR-1998;
20-MAR-1998;
                                                                                                                                                                                                                                                                                                                      Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
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28-MAY-1998;
28-MAY-1998;
30-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function: Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ43438, and AAX41685 to AAX41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
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                                                                                 LGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLNHA
                                                                                                                                                                                 VTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYH
                                                                                                                                                                                                            LCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKR
                                                                                                                                                                                                                                                      AVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATS
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98US-0087208.
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Pred. No. 6e-186;
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N-PSDB;
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03-AUG-1999;
09-SEP-1999;
01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; serine protease; osteopathic; immunosuppressive; antiallergic; antiinflammatory; cytostatic; cardiant; neuroprotective; nootropic; neuroleptic; vulnerary; opthalmological; antibacterial; antiviral; antifungal; antiparasitic; gene therapy; diagnosis; prevention; glaucon treatment; bone formation disorder; osteoporosis; arthritis; cancer; connective tissue disorder; autoimmune disorder; wound healing; asthma; systemic lupus erythematosus; male reproductive system disorder; systemic lupus erythematosus; male reproductive system disorder; arrhythmia; testicular cancer; digestion and food absorption disorder; arrhythmia; Crohn's disease; neurodegenerative disease; Alzheimer's disease; allerg behavioral disorder; Tourette's syndrome; acute myelogenous leukaemia; cardiovascular disorder; occular disorder; drug screening.
   The present sequence HCHAK72 (ATCC Deposit
                                                                                                                                                                            New nucleic acid molecules encoding human serine protease polypeptides useful for diagnosis, prevention and/or treatment of disorders e.g. osteoporosis, lupus erythematosus and Alzheimer's -
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   pman serine protease
PTA27).
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Best Local Similarity 100.0%;
Matches 327; Conservative
                                                                             Transmembrane serine protease; TADG-12; chromosome 17; vaccination; tumour associated differentially-expressed gene 12; cytostatic; hum malignant hyperplasia; cancer; ovary; breast; lung; colon; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissues in biological samples, identification of male contraceptive agents, delivery of compositions to targetted cells expressing a receptor for serine protease, hybridisation probes and molecular weight markers. Serine protease nucleic acids are also useful in gene therapy. Note: The present sequence shown in page 280-281 of sequence listing has been assigned SEQ ID NO: 14. But the sequence, human serine protease epidermal growth factor (EGF)-like domain (AAY/21:14) shown in page 12 is also referred as SEQ ID NO: 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferative and cancerous conditions (acute myelogenous leukaemia), allergic reactions (asthma), cardiovascular disorders (arrhythmia), occular disorders (glaucoma) and infectious diseases caused by bacteria, viruses, fungi or parasites. It is also useful for screening therapeutic compounds. Serine proteases are used as immunological probes or polymorphic markers for the identification of chromosomes, cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disorders (systemic lupus erythematosus), wound healing, reproductive system disorders (testicular cancer), digestion and for absorption disorders (crohn's disease), neurodegenerative diseases (Alzheimer's disease), behavioral disorders (Tourette's syndrome),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human serine proteases and their cDNA clones. It is used in methods for the diagnosis, prevention and treatment of various disorders related to serine protease such as bone formation disorders (osteoporosis), connective tissue disorders (arthritis),
                                                                                                                                                 Tumour associated differentially-expressed
                                                  Homo sapiens
                                                                                                                                                                                    11-JAN-2001
                                                                                                                                                                                                                                                    AAB32247 standard;
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Pred. No. 1.4e-135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC This invention relates to a novel transmembrane serine protease called CC tumour associated differentially-expressed gene 12 (TADG-12). TADG-12 is clocated on chromosome 17. Sequences AAA93842-A93845 and AAB32246-B32249 CC located on chromosome 17. Sequences AAA93842-A93845 and AAB32246-B32249 CC represent human TADG-12 (TADG-12V) leads to a truncated protein sequences. CC A splice variant of TADG-12 (TADG-12V) leads to a truncated protein CC product. TADG-12 is overexpressed in ovarian carcinomas. TADG-12 (CAXIADITES CONTROLLAR) and protein sequences are used in the CC diagnosis of malignant hyperplasia and cancers or the ovary, breast. CC lung, colon, prostate and other cancers where TADG-12 is overexpressed. CC TADG-12 is particularly used as tumour marker for early disease CC diagnosis. TADG12 proteins or fragments can be used to vaccinate an CC individual with cancer, suspected of having a cancer or at risk of CC getting cancer. Sequences AAA93846-A93853 represent PCR primers used for 2 amplifyIng the TADG-12 CDNA sequence, and in the quantitative analysis of CC TADG-13 marka. AAB3250 represents a peptide fragment of TADG-12, used to CC TADG-13 peptides which target HLA, and may be used in a vaccine or for immune stimulation.
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                                             AAB43572 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA fragment encoding tumor associated differentially-expressed gene protein used for diagnosing and treating malignant hyperplasia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAR-1999;
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                                                                                                                                                                                                                                               ftaaswktmcsddwkghyanvacaqlgfpsyvssdnlrvsslegqfreefvsidhllpdd
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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88.1%;
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Pred. No. 7.8e-101;
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IQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSE

329 63 Query Match
Best Local Similarity
Matches 245; Conserv

Conservative

0,

Mismatches

Indels Length

0

Gaps

0

54.7%;

Score 1339; DB 2; Pred. No. 1e-99;

DB 21; 0;

210

g

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AAC77607 to AAC78448 encode the human cancer associated proteins given CC in AAB4398 to AAB44239. The proteins can have activities based on the ctissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; contininfammatory; antithyroid; antiallargic; antibacterial; antiviral; comparison contrological; neuroprotective; cardiant; thrombolytic; coaquiant; contrologic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. CC polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating confiniting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoiamnune cells, nodulate haemostatic or thrombolytic activity, modulate
                                                          inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolyttlo; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 1598-1599; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acids comprising sequences encoding useful for treating or diagnosing e.g. cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer associated gene; cancer diagnosis; cytostatic; proliferative; antidiabetic; antiasthmatic; antirheum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-587533/55.
N-PSDB; AAC77781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200055350-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haemostatic; thrombol; neurological disease;
                                        the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen CA, Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer associated protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombolytic; cardiovascular disorder; infection; disease; drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US05882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vulnerary; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen; detection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO:1017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiviral;
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Query Match Best Local :

Similarity

42.3%; 100.0%;

Score 1034; DB 22; Pred. No. 2.2e-75;

Length

193;

0,

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RESULT
AAG73966
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                                                                       expression. For example, N and P may be used to treat discorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. By inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                             cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P
                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-SEP-2001
                                                               present invention.
                                                                                                                                                                                                                                                                  AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                     Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                     Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG73966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG73966 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330
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                                                   Pages
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                                                                                                                                                                                                                                                                                            11; Page 6530-6531;
                                                                                                                                                                                                                                                                                                                                                                                                     MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              colon cancer antigen protein SEQ ID NO:4730
                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                  acids encoding 4277 human
                                                                                                                                                                                                                                                                                                                                                             AAH33397
                       666 to 682 and page 7053 of the time of publication, meaning no 1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454
                                                                                                                                                                                                                                                                                                                     preventing,
                                                                                                                                                                                                                                                                                                                                                                                                    Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0157137.
99US-0163280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                               SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                    diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                    Birse CE,
                                                                                                                                                                                                                                                                                         9803pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193
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                                                                                                                                                                                                                                                                                                                     colon cancer-associated polypeptides,
and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                    Rosen
                                                                                                                                                                                                                                                                                                                                                                                                    CA;
                                    sequence listing were 
sequences are present
                                                                                                                                                                                                                                    and proteins (P), where cancer antigens. The colon
                                    present
                                    for
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Sequence

193

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                   This protein is encoded by a gene which is androgen (e.g. testosterone) inducible in androgen-dependent prostate cancer cells (e.g. LNCaP cells) and constitutively expressed in androgen-independent prostate cancer cells (e.g. LN INCaP cells). Agents which decrease the expression or activity of these clones may slow or arrest the growth of prostate cancer cells or may kill them. HrPCa6/7 can be obtained from the sequence of the known gene for TMPRSS2. A compound useful for treating prostate cancer can be identified in a novel method comprising measuring the expression level, or activity, of HRPCa2, 3, 6/7, 8, 9, 10, 13, 14, 15, 19, or peripheral-type benzodiatepine receptor (PBR) in a cell, in the presence and absence of a test compound. The sequences may also be used in diagnosis of prostate cancer and to determine efficacy of treatment
                                                                                                                                                                                                                                       Novel methods for identifying compounds for a comprising measuring the level of expression of 11 genes or their products
                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-1998;
30-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Androgen inducible; TMPRSS2; diagnosis.
                         for prostate cancer
                                                                                                                                                                                                                                                                                              N-PSDB; AAA08803
                                                                                                                                                                                                                                                                                                                                     Macbeth KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                30-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HrPCa6/7 polypeptide from androgen-inducible gene clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY92050 standard; Protein; 492 AA.
                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445
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4 heqmerdlkt 193
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                                                                                                                                                                                                               2; Fig 3; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inducible;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                    Shyjan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        98US-0163759
98US-0164159
                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US22535
                                                                                                                                                                                                                                                                                                                                     AW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     testosterone; prostate cancer; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                    compounds for treating prostate l of expression or activity of 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                     or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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δÃ

Matches

189;

Conservative

53;

Mismatches

149;

Indels Length

Gaps

11;

107

492; 21;

Query Match Best Local Similarity

35.8%; Score 876.5; DB 21; 45.9%; Pred. No. 2.9e-62;

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                                                                                                                                        Xu J, Dil
Kalos MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM01315 standard; Protein;
                      Claim 2; Page 539-540;
                                                            New polynucleotide encoding diagnosing, monitoring and t
                                                                                                   WPI; 2001-425873/45
                                                                                                                                                                                                       14-JAN-2000; 2000US-0483672
                                                                                                                                                                                                                                 16-JAN-2001; 2001WO-US01574
                                                                                                                                                                                                                                                          19-JUL-2001.
                                                                                                                                                                                                                                                                                    WO200151633-A2
                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                     cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                 Human; prostate
                                                                                                                                                                                                                                                                                                                                                                          P1000C amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                              AAM01315
                                                 for use in vaccines
                                                                                                                           Wang A,
                                                                                                                                                                              (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 VRVGGQNAVLQVFTA--ASWKTMCSDDWKGHYANVACAQLGFP-SYVSSDNLRVSSLEGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 ltlgtflvgaalaagllwkfmgskcsnsgiecdssgtcinpsnwcdgvshcpggedenrc 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYS--SRIVGGNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \verb|alpgawpwqvslhvqnvhvcggsiitpewivtaahcvekplnnpwhwtafagilrqsfmf|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCV-YDLYLPKSWTIQVGLV--SLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQMERD 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isgwgatee-kgktsevlnaakvllietgrcnsryvydnlitpamicagflqgnvdscqg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSGWGATEDGAGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQG
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                                                                                                                                        Dillon DC, Mitcham MD, Fanger GR, Day
                                                                                                                           Meagher MJ;
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                     cancer; prostate-specific;
e therapy; metastasis.
                     543pp; English
                                                                                                                                        CH,
                                                            g a prostate-specific protein,
treating prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                      492
                                                                                                                                        Harlocker SL, Jiang Retter MW, Stolk JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                 diagnosis; vaccine
                                                                                                                                                   Jiang Y,
                                                                                                                                       , Reed
Skeiky
                                                            for
patient
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                                                                                                                                        SG;
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The present invention describes polynucleotide sequences (I) which encode

06-JAN-2000

29-JUN-1999;

29-JUN-1998;

98US-0091044 99WO-US14622 Homo sapiens gene therapy;

WO200000605-A1

Tumour suppressor gene; TMPRSS2; cancer;

protein therapy

Human tumour suppressor TMPRSS2

polypeptide

human; drug design;

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RESULT 11
AAY77726
ID AAY777
В
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Best Local
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                                                                                                                                                                                                                                                         12-MAY-2000
                                                                                                                                                                                                                                                                                       AAY77726;
                                                                                                                                                                                                                                                                                                                        AAY77726 standard; Protein; 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 ltlgtflvgaalaagllwkfmgskcsnsgiecdssgtcinpsnwcdgvshcpggedenrc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCV-YDLYLPKSWTIQVGLV--SLLD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYS--SRIVGGNM 222
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45.9%;
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Pred. No. 2.9e-62;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                             AAY44406 standard; Protein; 492
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N-PSDB; AAZ87786.
WO9962942-A2
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                                                                                                                                    20P1F12; TMPRSS2; androgen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fmklntsagnv---diykklyhs----dacsskavvslrciacgvnlnssrqsrivgges
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tavtigian
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                                                                                                                                                                                                                                              (first entry)
                                                                                                   ss2; androgen; serine protease; 20P1F12-GTC1;
protein; colon; prostate; prostate tumour,
                                                                                                                                                                                         protein
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45.9%;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein) which is a prostate-specific, androgen-regulated, cell surface serine protease. It is a glycosylated type II transmembrane protein with an extracellular C-terminal serine protease domain, a scavenger receptor cysteine-rich domain, an LDL receptor class A domain and a predicted transmembrane domain. Host cells can be transformed to produce this protein, using vector containing 20PIF12/TMMPRSS2 gene (also designated 20PIF12-GTC1, as deposited with ATCC accession number 207097). Anti-20PIF12/TMMPRSS2 antibodies may be used as therapeutic agent for prostate and colon cancers, to image prostate cancer cells and prostate tumours, to identify ligands and cellular constituents that bind to a 20PIF12/TMMPRSS2 gene product and for use as cancer vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998;
29-JUN-1998;
14-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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(SAFF/)
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                                                                                                                                                                                                                                                                                                                                                                  52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence is the 20P1F12 protein (also known as the TMPRSS2
                                                                                                                                                                                                                                                                                                                                                       IVIGIIALILALAIGLGIHF---DCSGK-YRCRSSFKCIELIARCDGVSDCKDGEDEYRC
              DSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQMERD
                                                                    TSGWGATEDGAGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQG
                                                                                                          yga-gyqvekvishpnydsktknndialmklqkpltfndlvkpvclpnpgmmlqpeqlcw
                                                                                                                                                                                SLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCV-YDLYLPKSWTIQVGLV--SLLD:| ||| || | | || || ||: ||: ||:
                                                                                                                                                                                                                                        FREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYS--SRIVGGNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-116363/10
dsggplvtsknniwwligdtswgsgcakayrpgvygnvmvftdwiyrqmrad
                                                                                                                                       NPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCW: 339
                                                                                                                                                                  alpgawpwqvslhvqnvhvcggsiitpewivtaahcvekplnnpwhwtafagilrqsfmf
                                                                                                                                                                                                                                                                              vrlygpnfilqvyssqrks \verb|whpvcqddwnenygraacrdmgyknnfyssqgivddsgsts|
                                                                                                                                                                                                                                                                                                           VRVGGQNAVLQVFTA--ASWKTMCSDDWKGHYANVACAQLGFP-SYVSSDNLRVSSLEGQ 164
                                                                                                                                                                                                                                                                                                                                     ltlgtflvgaalaagllwkfmgskcsnsgiecdssgtcinpsnwcdgvshcpggedenrc 148
                                                       isgwgatee
                                                                                                                                                                                                                        fmklntsagnv---diykklyhs----dacsskavvslrciacgvnlnssrqsrivgges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) UROGENESYS INC.
) AFAR D E.
) HUBERT R S.
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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SAFFRAN D C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 492
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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98US-0091474.
99US-0129521.
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45.9%;
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                                                                                                                                                                                                                                                                                                                                                                                          Score 875.5; DB 21;
Pred. No. 3.5e-62;
53; Mismatches 149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate-specific proteins (II). (I) and (II) have cytostatic activity and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies is prostate cancer. (I) and (II) can be used in vaccines in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosing, monitoring and for use in vaccines -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xu J,
Kalos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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LQFQGYHLCGGSVITPLWIITAAHCV-YDLYLPKSWTIQVGLV--SLLDNPAPSHLVEKI
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                                                                                                                                                                                     LPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYS--SRIVGGNMSLLSQWPWQAS
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Meagher MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393 AA;
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GR, Day
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46.6%;
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Pred. No. 9.
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Matches Query Match Best Local

186;

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55;

Score 864.5; I Pred. No. 2.6e-55; Mismatches

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30-AUG-1999;
30-DEC-1999;
24-JAN-2000;
                                                                                                                                                     The present invention relates to prostate specific androgen regulated proteins. The invention may be used to determine an expression level of the prostate-specific proteins ARSDRJ, TWPRSZ2, or PART-1 in a fluid sample or prostate cell sample from an individual. It may also be used for diagnosing and predicting the susceptibility of a prostate neoplastic condition in an individual. Inhibitors of the proteins are useful for treating or preventing the progression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide encoding prostate specific androgen regulated polypeptides and inhibitor of the peptides useful for treating reducing the progression of prostate neoplastic condition in individual -
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 63; Page 86-88;
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99US-0151585.
99US-0174003.
2000US-0177751.
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The invention relates to detecting, diagnosing metastasis and staging cancer by measuring levels of cancer specific genes (CSG) in cells, tissues or body fluids. Their remission and progression, decreases and increases in CSG levels, is also monitored, by periodic sample analysis. The methods are useful for detecting cancers, especially gynecologic cancers which include ovarian, breast, endometrial and uterine cancer and lung cancer. Antibodies against the CSGs labeled with paramagnetic ions or a radioisotope is useful for imaging cancer and when conjugated
                                                                                                                                              Diagnosing, staging, monitoring, imaging and treating cancer especially gynecological cancers e.g. breast, ovarian cancer and lung cancer, involves measuring cancer specific gene levels in cells and body fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ovrl15 homolog protein
                                                                                                             Disclosure; Page 52-54; 58pp; English.
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N-PSDB; AAZ90478.
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                                                                                                                                                                                                                                                                                                                                                          with a cytotoxic agent are useful for treating cancer. The present sequence represents a Ovrll5 homolog protein, that can be used for the detection of the various cancers.
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                       149
440
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                                                                                                                                                                                                                                              89
                                                                                                                                                                                                                                                        Local Similarity 45.4
nes 186; Conservative
                                                                                                                    DSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME 449
                                                                            yga-gyqvqkvishpnydsktknndialmklqkpltfndlvkpvclpnpgmmlqpeqlcw
                                                                                        vrlygpnfilqmyssqrkswhpvcqddwnenygraacrdmgyknnfyssqgivddsgsts
                                                                                                                                                                                                               VRVGGQNAVLQVFTA--ASWKTMCSDDWKGHYANVACAQLGFP-SYVSSDNLRVSSLEGQ
dsggplvtsnnniwwligdtswgsgcakayrpgvygnvmvftdwiyrqmk
                                      isgwgatee-kgktsevlnaakvllietqrcnsryvydnlitpamicagflqgnvdscqg
                                                  TSGWGATEDGAGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQG
                                                                                                                                                                                                                                            {\tt ltlgtflvgaalaagllwkfmgskcsnsgiecdssgtcinpsnwcdgvshcpggedenrc}
                                                                                                                                                                                                                                                                                                                                         492 AA;
                                                                                                                                                                                                                                                                                                35.3%;
                                                                                                                                                                                                                                                                                     55;
                                                                                                                                                                                                                                                                                               Score 864.5;
Pred. No. 2.6
                                                                                                                                                                                                                                                                                       Mismatches
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Search completed: Job time: 84 sec April 11, 2002, 08:53:56

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             April 11, 2002, 08:52:32; Search time 28.67 Seconds (without alignments) 2316.276 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                       473505 seqs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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2447
sp_phage:*
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sp_bacteria:*
sp_fungi:*
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sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	80	7	6	u	4	ω	N	1	No.	Result	
533	533	537	537.5	539	539	539	539	542.5	548.5	564	564.5	567	568	579	712.5	728	825.5	875.5	Score		
21.8	21.8	21.9	22.0	22.0	22.0	22.0	22.0	22.2	22.4	23.0	23.1	23.2	23.2	23.7	29.1	29.8	33.7	35.8	Match Length	Ouerv	¥Ρ
855	529	855	845	2382	1462	1449	1186	855	868	1322	418	1322	799	643	537	581	767	492	Length 1		
4	4	4	13	ഗ	σ	G	G	11	G	Ç	4	υ	11	σ	4	4	13	4	DB		
Q9HCA3	Q9BS01	Q9H3S0	Q9DGR1	Q9BI19	Q9U1I3	Q9U112	Q9VSU2	Q9JJI7	Q9Y1V3	Q9NATO	060235	Q9NJS5	Q9DBIO	097506	Q9BYE1	Q9BYE2	Q9DGR2	Q9BXX1	ID		
homo	Q9bs01 homo sapien	Q9h3s0 homo sapien	Q9dgrl xenopus lae	Q9bil9 drosophila	Q9uli3 drosophila	Q9uli2 drosophila	Q9vsu2 drosophila	Q9jji7 rattus norv	Q9y1v3 polyandroca	Q9nat0 anopheles q	060235 homo sapien	Q9njs5 anopheles g	Q9dbi0 mus musculu	097506 sus scrofa	Q9byel homo sapien	Q9bye2 homo sapien	Q9dgr2 xenopus lae	Q9bxx1 homo sapien	Description		

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				19.8	19.8	19.8	19.9	20.2	20.2	20.2	20.3	20.3	20.4	20.4	20.4	20.4	20.7	20.7	20.7	20.8	20.9	20.9	20.9	20.9	21.5
264	260	275	421	282	502	454	273	749	571	325	317	273	339	334	329	806	810	624	311	389	812	581	422	310	279
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Q9eqz8 rattus norv	Q9w7q3 paralichthy	Q15661 homo sapien	Q60491 cavia porce	Q9d4i3 mus musculu	Q9cw97 mus musculu	O46506 papio hamad	Q9xsm1 ovis aries	Q99jc8 rattus norv	Q9y495 homo sapien	015944 sarcophaga	Q9dgr3 xenopus lae	Q9xsm2 ovis aries	Q99144 mus musculu	046507 papio hamad						Q9pvx7 xenopus lae	Q9r0w3 rattus norv	Q9xzm7 strongyloce	Q9u152 homo sapien		Q9qz74 rattus norv

ALIGNMENTS

Оу	рь о _у	M B Q	SQ.	FT	K C	RL	RA	7 F	RL	RT	RT	RA :	RA	RX:	R A	U (2 6	88	SO	GN	DE	Di	7	DI.	AC		RESULT
108 VRVGGQNAVLQVFTAASWKTMCSDDWKGHYANVACAQLGFP-SYVSSDNLRVSSLEGQ 164	52 IVIGIIALILALAIGLGIHFDCSGK-YRCRSSFKCIELIARCDGVSDCKDGEDEYRC 107 : :	Query Match 35.8%; Score 875.5; DB 4; Length 492; Best Local Similarity 45.9%; Pred. No. 6.1e-74; Matches 189; Conservative 53; Mismatches 149; Indels 21; Gaps 11;	CRC64;	CHAIN 256 492 ANDROGEN-REGULATED SERINE PROTEASE	EMBL; AF2/0487; AAX29280.1;	(MAY-2000) to the	Mitchell S.C., Hubert R.S., Afar D.E.H.;	SECTION OF A	cer Res. 61:1686-1692(2001).	epithelia.";	"Catalytic cleavage of the androgen-regulated TMPRSS2 protease results		Afar D.E.H., Vivanco I., Hubert R.S., Kuo J., Chen F., Saffran D.C.	MEDLINE-21139112; pubMed-11245484;	SPOTENCE FROM N A	[1]	Mammala; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Chordata; Craniata; Vertebrata; E			GULATED SERINE PR	(TrEMBLiel.	(Tremaine) 17	01-JUN-2001 (TrEMBLrel. 17, Created)	•	Q9BXX1 PRELIMINARY; PRT; 492 AA.	ILT 1

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                                                                                                  Query Match
Best Local Similarity
Matches 175; Conser
                                                                                                                                                                                                                       PRINTS; PRO072; CHYMOTRYPSIN.
PRINTS; PRO072; CHYMOTRYPSIN.
SMART; SM00192; LDLa; 8.
SMART; SM00202; SR; 1.
SMART; SM00202; Tryp_SPc; 1.
SMART; SM00206; Tryp_SPc; 1.
SMART; PS00034; LDLRA_2; 2.
PROSITE; PS000134; TRYPSIN_HIS; UNKNOWN_1.
Glycoprotein; Hydrolase; Protease; Serine protease.
SEQUENCE 767 AA; 86001 MW; E0566A38796DE96E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: TO SERINE PROTEASES, TR
-!- SIMILARITY: TO CHYMOTRYPSIN SERINE
EMBL; AB038497; BAB08217.1; -
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002172; LDL_recept_A.
InterPro; IPR001190; SRCR.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-20363741; PubMed-10903452;
Yamada K., Takabatake T., Takeshim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XESP-2.
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17, EMBRYONIC SERINE PROTEASE-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9DGR2;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00057; ldl_recept_a; Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene
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     394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amada K., Takabatake T., Takeshima K.;
ISolation and characterization of three no
rom Xenopus laevis.";
ene 252:209-216(2000).
I- SIMILARITY: TO LOW DENSITY LIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    440
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                                                  78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LDLRA) DOMAIN
                             RCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVF--TAASWKTMCSDDWKG
RCGSSVSCVLSSQWCDGVSDCPYGEDEMSCVSLYPADFQLQVYSTSVSAWLPVCSDYWND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSGGPLVTSKNNIWWLIGDTSWGSGCAKAYRPGVYGNVMVFTDWIYRQMRAD
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                                                                                                     Conservative
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                                                                                                                             33.7%;
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Last sequence up
Last annotation
                                                                                               Score 825.5; DB 13
Pred. No. 5.7e-69;
6; Mismatches 131;
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Best Local Similarity
Matches 157; Conser
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01-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                       Protease.
SEQUENCE
                                                                                                                                                                                                                                                                                                                              *Rim D.R., Sharmin S., Inoue M., Kido H.;

"Cloning and expression of novel mosaic serine without a transmembrane domain from human lung. Biochim. Biophys. Acta 1518:204-209 (2001).

EMBL; AB048796; BAB39741.1;
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01-JUN-2001 (TrembLrel.
01-JUN-2001 (TrembLrel.
MEMBRANE-TYPE MOSAIC SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BYE2
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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 276
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|:| ||| ||| || ||:||:||: ||
SWGDGCARANKPGVYGNVTTFLEWIYSQM 763
                                                                                                                                LKSDELGCVRFDWDKSLLKIYSGSSHQWLPICSSNWNDSYSEKTCRQLGFESAHRTTEVA
 SLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDG
                         VGGALASDSKWPWQVSLHFGTTHICGGTLIDAQWVLTAAHCFFVTREKVLEGWKVYAGTS
                                                  VGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDL--YLPKSWTIQVGLV
                                                                                                   VSSLEGQFREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRI
                                                                                                                                                DGEDEYRCVRVGGQNAVLQVFTAAS--WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLR 157
                                                                                                                                                                                  LPL-----IGCVLLLIALVVSLIILFQFWQGHTGIRHKEQRESCPKHAVRCDGVVDCK
                                                                                                                                                                                                            LPLKFFPIIVIGIIALILALAIGLGIHFDC----SGKYRCRSSFKCIELIARCDGVSDCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAIPLIDSNVCNQSYVYNGQITSSMICAGYLSGGVDTCQGDSGGPLVNKRNGTWWLVGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYDNDIALMKLRDEITFGYTTQPVCLPNSGMFWEAGTTTWISGWGSTYEG-GSVSTYLQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVITPLWIITAAHCVYDLYLPKS-WTIQVGLVSLLDNP----APSHLVEKIVYHSKYKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSSY----CYSGNVVSLHCISCGVSNNSLVSRIVGGTFANLGNWPWQVNLQYITGVLCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSVYVREGCASGHVVTLQCTACG-HRRGYSSRİVGGNMSLLSQMPMQASLQFQGYHLCGG
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                                                                          -HRDFANSFSILRYN--STIQESLH-RSHCPSQRYISLQCSHCG-LRAMTGRI
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Primates;
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Last sequence up
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Pred.
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                                                                                                                                                                                                                                       Mismatches
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No. 6e-60;
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Best Local Sin
Matches 145;
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Q9BYE1;
01-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21167393; PubMed-11267681; Kim D.R., Sharmin S., Inoue M., Kido H.; "Cloning and expression of novel mosaic serine without a transmembrane domain from human lung. Biochim. Biophys. Acta 1518:204-209(2001).

EMBL; AB048797; BAB39742.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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Mammalia; Eutheria;
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                                                        LDWIHEQMERDLK
                                                                                     TPRMMCAGDLHGGRDSCQGDSGGPLVCEQNNRWYLAGVTSWGTGCGQRNKPGVYTKVTEV
                                                                                               HPACLPMHGQTFSLNETCWITGFGKTRETDDKTSPFLREVQVNLIDFKKCNDYLVYDSYL
                                                                                                                                            QPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLNHAAVPLISNKICNHRDVYGGII
                                                                                                                                                                                     --YLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMI
                                                                                                                                                                                                                    CPKHAVRCDGVVDCKLKSDELGCVRFDWDKSLLKIYSGSSHQWLPICSSNWNDSYSEKTC
                                                                                                                                                                                                                                                                                                                       CIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAAS--WKTMCSDDWKGHYANVAC
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                                                                                                                                                                                                                                          QCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDL
                                                                                                                                                                                                                                                                RQLGFESAHRTTEVA------HRDFANSFSILRYN--STIQESLH-RSHCPSQRYISL
                                                                                                                                                                                                                                                                                   AQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTL
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                                          LPWIYSKMESEVR
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Primates;
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Last annotation updat
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4; Mismatches
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Pred. No. 1.
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Best Local Similarity
Matches 128; Conser
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; PAN.
InterPro; IPR001254; Trypsin.
InterPro; IPR001254; Trypsin.
InterPro; IPR001254; Trypsin.
InterPro; IPR001254; APPLEDOMAIN.
Pfam; PF000089; trypsin; 1.
PFRINTS; PR00005; APPLEDOMAIN.
PRINTS; PR000123; APPLE; 4.
SMART; SM00223; APPLE; 4.
SMART; SM00223; APPLE; 4.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNO
PROSITE; PS00135; TRYPSIN_HIS; UNKNO
PROSITE; PS00135; TRYPSIN_HIS; UNKNO
Q9DBIO
Q9DBIO;
01-JUN-2001
01-JUN-2001
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Eukaryota; Metazoa; C
Mammalia; Eutheria; C
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              097506
097506;
01-MAY-1999
01-MAY-1999
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; S01.212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                            590
                                                                                                                 405
                                                                                                                                       534
                                                                                                                                                                                     474
                                                                                                                                                                                                            287
                                                                                                                                                                                                                                   414
                                                                                                                                                                                                                                                        232
                                                                                                                                                                                                                                                                                361
                                                                                                                                                                                                                                                                                                       177
                                                                                                                                                                                                                                                                                                                             309
                                                                                                                                                                                                                                                                                                                                                    132
                                                        σ
                                                                                                        LVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQMERD
                                                                                            LVCKYNGIWHLVGTTSWGEGCARREQPGVYTKVIEYMDWILEKTQDD
                                                                                                                                                                                    VKEIIHQNYKILESGHDIALLKLETPLNYTDFQKPICLPSRDDTNVVYTNCWVTGWGFT
                                                                                                                                                                                                 VEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGAT
                                                                                                                                                                                                                                  VSLQAKLRAQNHLCGGSIIGHQWVLTAAHCFDGLSLPDIWRIYGGILNISEITKETPFSQ
                                                                                                                                                                                                                                                                                            PDDKVTALHHSVYVREG-----CASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQ
                                                                                                                                                                                                                                                                                                                                                   DWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSID-------HLL 176
                                                                                                                                       EE-KGEIQNILQKVNIPLVSNEECQKSYRD---HKISKQMICAGYKEGGKDACKGESGGP
                                                                                                                                                              EDGAGDASPVLNHAAVPLISNKIC--NHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGP 404
                                                                                                                                                                                                                                                       ASLQFQ----GYHLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGL--VSLLDNPAPSHL
                                                                                                                                                                                                                                                                               SDGSPTKITHGMRASSGYSLRLCRSG-----DHSACATKA--NTRIVGGTDSFLGEWPWQ
                                                                                                                                                                                                                                                                                                                             DFEGEELNV-----TFVQGANLCQETCTKTIRCQFFTYSLHPEDCRGEKCKCSLRLS
                                                                                                                                                                                                                                                                                                                                                                                                                                   Serine protease.
643 AA; 72227 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TrEMBLrel.
TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                   23.7%; Score 36.9%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10,
10,
17,
                                                                                                                                                                                                                                                                                                                                                                          55;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; UNKNOWN_1:
                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AFF2923E3C3CB80A CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   579;
No. 7
                                   799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               643
                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                   AA
                                                                                                                                                                                                                                                                                                                                                                          118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                   451
                                                                                            636
                                                                                                                                                                                                                                                                                                                                                                                                 643;
                                                                                                                                                                                                                                                                                                                                                                          46;
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                         286
                                                                                                                                                                                     533
                                                                                                                                                                                                           346
                                                                                                                                                                                                                                   473
                                                                                                                                                                                                                                                                                                      231
                                                                                                                                                                                                                                                                                                                            360
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10;

(TrEMBLrel.

17, 17,

Last sequence update)

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В
                                                                                                                                                                                                                                                                                                                                                                                  Db
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubii F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Fruuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Hayashi-Poris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00057; Idl_recept_a; 3.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR007261; LDLRECEPTOR.
SMART; SM00042; CUB; 1.
SMART; SM00192; LDLa; 3.
SMART; SM00192; LDLa; 3.
SMART; SM00192; Tryp_SPC; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS0134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS04068; LDLRA_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
-!- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
EMBL; AK004939; BAB23684.; -.
MGD; MGI:1919003; 1300008A2ZRik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=LIVER;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000859; CUB.
InterPro; IPR002172; LDL_recept_A.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 1300008A22RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1300008A22RIK.
                                      210
                                                                                                         531
                                                                                                                                                                         150
                                                                                                                                                                                                                                            475
                                                                                                                                                                                                                                                                                                               105
                                                                                                                                                                                                                                                                                                                                                                                  418
                                                                                                                                                                                                                                                                                                                                                                                                                                                 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LDLRA) DOMAIN
RRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYD--LYLPKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVIGIIALILALAIGLGIHFD------CSGKYRCRSSFKCIELIARCDGVSDCKDGEDE 104
                                                                                                      CVKKPN---PECDGQ-
                                                                                                                                                                  YVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGH
                                                                                                                                                                                                                                                                                                           YRCVRVGGQNAVLQV---FTAASWKTMC-----SDDWKGHYANVACAQLGFP----S
                                                                                                                                                                                                                                                                                                                                                                              VTINFTSQISLTGPGVQVYYSLYNQSDPCPGEFLCSVNGLC---VPACDGIKDCPNGLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                            -CRAMFQCQEDSTCISLPRVCDRQPDCLNGSDEEQCQEGVPCGTFTFQCEDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 568; DB 11;
Pred. No. 1.1e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                      ---SD-----CRDGSDEQH-----CD-CG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e protease.
16315A646A4D5288 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LDL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                  474
                                   267
                                                                                                                                                                     209
                                                                                                                                                                                                                                                                                                           149
                                                                                                                                                                                                                                        530
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δõ

Query Match

23

. 28;

Score

567;

DВ

5;

Length 1322;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                       InterPro; IPR002172; LDL_recept_A.
InterPro; IPR001190; SRCR.
InterPro; IPR001254; Trypsin.
InterPro; IPR001254; Trypsin.
Pfam; PF01607; Chitin_bind_2; 2.
Pfam; PF00057; ldl_recept_a; 2.
Pfam; PF000530; SRCR; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00258; SPERACTRCPTR.
PRINTS; PR00258; SPERACTRCPTR.
PRINTS; PR00258; SPERACTRCPTR.
                                          PROSITE; PROSITE;
                                                                  PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                 Anopheles gambiae hemolymph.";
Insect Biochem. Mol. Biol. 30:35-46(2000).
-!- SIMILARITY: TO LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR CLASS
  Glycoprotein;
SEQUENCE 13
                                                                                                         SMART; SM00202;
SMART; SM00020;
                                                                                                                                  SMART; SM00494; ChtBD2; SMART; SM00192; LDLa; 2
                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY:
-!- SIMILARITY:
EMBL; AF117751;
                                                                                                                                                                                                                                                                                                                                                                                              Gorman M.J., Andreeva O.V., Paskewitz "Molecular characterization of five se Anopheles gambiae hemolymph.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000
01-JUN-2001
                           PROSITE;
                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20110889; PubMed=10646969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=G3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anopheles gambiae (African malaria mosquito)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SP22D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9NJS5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9NJS5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            558
                                                                                                                                                                                                                                                                                                                                                         (LDLRA) DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WIQQ 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WIHE 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLCAGYRKGKKDACQGDSGGPLVCREPSGRWFLAGLVSWGLGCGRPNFFGVYTRVTRVIN 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLCAGYLTGGVDSCQGDSGGPLVCQE-RRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLPARSHFFEPGQHCWITGWGAQREG-GPVSNTLQKVDVQLVPQDLCS--EAYRYQVSPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLNHAAVPLISNKICNHRDVYGGIISPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WTVFLG--KMRQNSRWPGEVSFKVSRLFLHPYHEEDSHDYDVALLQLDHPVVYSATVRPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTIQVGLVSLLDNP----APSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQGLSSRIVGGTVSSEGEWPWQASLQIRGRHICGGALIADRWVITAAHCFQEDSMASPKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEASE
PS01209; IDLRA_1; 1.

PS50068; LDLRA_2; 2.

PS00420; SRCR_1; UNKNOWN_1.

PS50287; SRCR_2; 2.

PS00134; TRYPSIN_HIS; UNKNOWN_1.

PS00135; TRYPSIN_SER; 1.

PS00135; TRYPSIN_SER; 1.

PS00135; TRYPSIN_SER; 1.

PS00135; TRYPSIN_SER; 2.

PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                             IPR002557; Chitin_binding
IPR001314; Chymotrypsin.
IPR002172; LDL_recept_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-HEMOLYMPH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                        SR; 2.
Tryp_SPc;
                                                                                                                                                                                                                                                                                                                  TO CHYMOTRYPSIN SERINE AAD38337.3; -.
                                                                                                                                                                                                                                                                                                                                            TO SERINE PROTEASES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endopterygota;
                                                                                                                                               2
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15,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                           serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1322
                                                                                                                                                                                                                                                                                                                                             TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                               PROTEASE FAMILY (S1)
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    CRC64;
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Best Local Similarity

31.3%;

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RESULT
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                                         InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001082; SEA.
InterPro; IPR001254; Trypsin.
InterPro; IPR001254; Trypsin.
Pfam; PF01390; SEA; 1.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00200; SEA; 1.
SMART; SM000200; SEA; 1.
SMART; SM000200; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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O60235; O1-AUG-1998 (TrEMBLrel. 07, Cre
O1-AUG-1998 (TrEMBLrel. 07, Las
O1-JUN-2001 (TrEMBLrel. 17, Las
AIRWAY TRYPSIN-LIKE PROTEASE.
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Yamaoka K., Masuda K., Ogawa H., Takagi K., Un
"Cloning and characterization of the cDNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1278
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                                                                                                                                                                                                                                                                                               MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                       Hydrolase;
                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIGITALILALAIGLGIHFDCSGKY-RCRSSFKCIELIARCDGVSDCKDGEDEY--RC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQMERDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QFREGHHMSNDIAVVVLKTPVRFNDYVQPICLPARDAPYLPGQNCTISGWGATEAGSKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEGGFREEFVSIDHLLP--DDKVTALHHSVYVREGCASGHVVTLQC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTLTGIVSWGKHCGYANKPGVYLKVAHYRDWIEQKLNQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYDLRAGTVPLLPDSVCRRPEVYGDSLIDGMFCAGTLEPGVDSCDGDSGGPLVCPNSEGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---VR-VGG---QNAVLQVFTAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KYKP-KRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDA
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S01.301; -.
Protease;
418 AA; 4
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46263 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
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Last sequence update)
Last annotation update)
                       protease
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8; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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F4BC1DB020CFBBD0
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or human airway
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Best Local S
Matches 142
InterPro; IPR002557; Chitin_binding.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR0013172; LDL_recept_A.
InterPro; IPR0012172; LDL_recept_A.
InterPro; IPR001254; Trypsin.
Pfam; PF01607; Chitin_bind_2; 2.
Pfam; PF00057; Idl_recept_a; 2.
Pfam; PF00057; Idl_recept_a; 2.
Pfam; PF00059; trypsin; 1.
PRINTS; PR00725; CHYMOTRYPSIN.
PRINTS; PR007258; SPERACTRCPTR.
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                     (LDLRA) DOMAIN.

-i- SIMILARITY: TO SERINE PROTEASES, TR
-i- SIMILARITY: TO CHYMOTRYPSIN SERINE
EMBL; AJ276428; CAB81934.1; -
                                                                                                                                                                                                                                                                                                                                                                                                   "A modular chitin-binding protease associated wi
hemolymph in the mosquito Anopheles gambiae.",
Proc. Natl. Acad. Sci. U.S.A. 97:7136-7141(2000)
-!- SIMILARITY: TO LOW DENSITY LIPOPROTEIN (LDL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-20318993; PubMed=10860981;
Danielli A., Loukeris T., Lagueux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADHESIVE SERINE PROTEASE SP22D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kafatos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles gambiae (African malaria mosquito).
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Last sequence update)
Last annotation updat
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Pred. No. 9.7e-45;
8; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tracheata; Hexapoda; Insecta;
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R SMART; SM00192; LDLa; 2.

JR SMART; SM00202; SR; 2.

JR SMART; SM00202; Tryp_SPc; 1.

JR PROSITE; PS01209; LDLRA_1; 1.

JR PROSITE; PS50068; LDLRA_2; 2.

DR PROSITE; PS500420; STCRL]; UNKNOWN_1.

DR PROSITE; PS50287; STCR_1; UNKNOWN_1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW Glycoprotein; Hydrolase; Protease; Serine protease.

SO SEQUENCE 1322 AA; 146794 MW; FBF973C21CC5475B CRC64;
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Best Local S
Matches 143
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Q9Y1V3;
Q1-NOV-1999
Q1-NOV-1999
Q1-JUN-2QQ1
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                                            ohashi M., Kawamura K., Fujii N., 1
"A retinoic acid-inducible modular
Dev. Biol. 0:0-0(1999).
-i- SIMILARITY: TO LOW DENSITY LIPO
                                                                                                                                         SEQUENCE FROM N.A. STRAIN-WHITE SPOT;
                                                                                                                                                                                                           Polyandrocarpa misakiensis.
Eukaryota; Metazoa; Chordata;
Stolidobranchia; Styelidae; Po
NCBI_TaxID=7723;
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                                                                                                                                                                                                                                                                                                             TRAMP
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(LDLRA) DOMAIN.
SIMILARITY: TO
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(TrEMBLrel 12, Last sequence update)
(TrEMBLrel 17, Last annotation update)
TINOIC ACID-INDUCIBLE MODULAR PROTEASE P
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  PROTEASES,
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                                                                                                                                                                                                                                        Polyandrocarpa
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Pred. No. 5.1e-44;
8; Mismatches 175;
                                                                                                                                                                                                                                                            Urochordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                              LIPOPROTEIN
                                                                                                                Yubisui
                                                                                        Yubisui T., protease in
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                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                      Qγ
                                                                                                                                                                                                                                    DЪ
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                                                                                                                                                                                                                                                                                                              γ
                                                                                                                                                                                                                                                                                                                                         В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                   日
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00202; SR; 2.

SMART; SM00202; Tryp_SPc; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS01020; LDLRA_1; 3.

PROSITE; PS50068; LDLRA_2; 3.

PROSITE; PS50034; TRYPSIN_HIS; UNKNOWN_1.

PROSITE; PS00134; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

SIGNAL

SIGNAL

SIGNAL

SIGNAL

SEQUENCE 868 AA; 97659 MW; F71462865F36A6CA CRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR001254; Trypsin.
Pfam; PF00057; ldl_recept_a; 3.
Pfam; PF000530; SRCR; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00261; LDLRECEPTOR.
PRINTS; PR00258; SPERACTRCPTR.
SMART; SM00192; LDLa; 3.
SMART; SM00473; PAN_AP; 1.
O9JJI7:
01-0CT-2000 (TrembLrel. 15, Created)
01-0CT-2000 (TrembLrel. 15, Last sequence update)
01-JUN-2001 (TrembLrel. 17, Last annotation update)
MEMBRANE BOUND SERINE PROTEASE (MEMBRANE BOUND ARGININE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART;
SMART;
SMART;
                                                                   Q9JJI7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003609;
InterPro; IPR001190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                   831
                                                                                                                                                           417
                                                                                                                                                                                     775
                                                                                                                                                                                                                                       715
                                                                                                                                                                                                                                                             307
                                                                                                                                                                                                                                                                                        656
                                                                                                                                                                                                                                                                                                                249
                                                                                                                                                                                                                                                                                                                                           596
                                                                                                                                                                                                                                                                                                                                                                                            548
                                                                                                                                                                                                                                                                                                                                                                                                                                               493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hes 146;
                                                                                                                                                                                                                                                                                                                                                                                                                     165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72
                                                                                                                                  GIVSWGNGCAKPKAPGVYAKVAVFIDWI-EQM
                                                                                                                                                 GATSFGIGCAEVNKPGVYTRVTSFLDWIHEQM
                                                                                                                                                                                    LMKLAGP----LTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDA-SPVLNHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DC--SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRC----VRVGGQNAV----LQVFT
                                                                                                                                                                                                                                                                                                                                                                                                                                             GRKYGLICDTRWSIREADVVCRQLGFRRGAIDALKGGAFGRIDRRYV-LDNVRCNG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DCAATNRYLCNDG-SCIEHDQVCDFRDDCPNGEEETECEPMKIRLRGGSGPFEGHVEVAK
                                                                                                                                                                                                                                     LLRIENDARECATITPEVQTVCLPKSSSQFDAKTICEVTGWGKDSATAVRAYVPVLQEAE
                                                                                                                                                                                                                                                                                        PCWVLTAAHCFVREYPIRDYTIRLGDHITGVDDETEQLFKIAEIIKHD-YNVTTKENDIA
                                                                                                                                                                                                                                                                                                               PLWIITAAHCVYDLYLPKSWTIQVG--LVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIA
                                                                                                                                                                                                                                                                                                                                          RRITTPTPPPMPECGRKPVIEAPLPTARIVGGSGTEPHEWPWQAGIWLPWTYWCGGSLIH
                                                                                                                                                                                                                                                                                                                                                                                            -REE--SLEN------CRHSGWNKASCSIDHEVGVICRQEATTPSPSPSATPQPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                   FREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AASWKTMCSDDWKGHYANVACAQLGF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB030007; BA.
P00750; 1RTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                         ----TACGHRRGY-----SSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LDLa; 3.
; PAN_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chymotrypsin.
LDL_recept_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan_app.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 548.5;
Pred. No. 8.
                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SERINE
                                                                    855
                                                                                                                                                           448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------PSYVSSDNLRVSSLEGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.3e-43;
nes 148;
                                                                    ζ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal
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     SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                     830
                                                                                                                                                                                                             416
                                                                                                                                                                                                                                                                                                                306
                                                                                                                                                                                                                                                                                                                                          655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                             361
                                                                                                                                                                                                                                                                                        714
                                                                                                                                                                                                                                                                                                                                                                                             595
                                                                                                                                                                                                                                                                                                                                                                                                                                             547
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                                                                                                                                                                                                                                                                                                                                                                                                           Matches 135;
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0261; LDLTRECEPTOR.
SMART; SM00042; CUB; 2.
SMART; SM00042; LDLa; 3.
SMART; SM00020; Tryp_SPc; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00339; AA TRNA LIGASE_II_2; UN
PROSITE; PS01180; CUB; 2.
PROSITE; PS01180; LDLRA_1; 2.
PROSITE; PS50168; LDLRA_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00431; (Pfam; PF00057; Pfam; PF00089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
VARIANT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2000) to the EMBL/GenBank/DDBJ day-i- SIMILARITY: TO LOW DENSITY LIPOPROTEIN (LDL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indue H., Takahashi K., Kishi K.;
"membrane-bound arginine specific serine protease.";
"membrane-bound arginine specific serine protease.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
Mammalia; !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A membrane bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SERINE PROTEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                             500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LDLRA) DOMAIN.

I SIMILARITY: TO SERINE PROTEASES, TRYPIS SIMILARITY: TO CHYMOTRYPSIN SERINE PROMBL; AB037898; BAB03502.1; -...

SMBL; AB049189; BAB03502.1; -...

SMBL; AB049189; BAB13765.1; -...

InterPro; IPR002106; AA_tRNA_ligase_II.

InterPro; IPR001314; Chymotrypsin.

InterPro; IPR001314; Chymotrypsin.

InterPro; IPR001272; LDL_recept_A.

InterPro; IPR001254; Trypsin.
   321
                                                                                         809
                                                                                                                                                   549
                                                                                                                                                                                 179
                                                                                                                                                                                                                                           133
                                                                                                                                                                                                                                                                       453
                                                                                                                                                                                                                                                                                                    73
QPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLNHAAVPLISNKICNHRDVYGGII
                             DHTMWTAFLGLLDQSKRSASGVQEHKLKRITHPSFNDFTFDYDIALLELEKPAEYSTVV
                                                                                                                                                                                                                                                                                          CSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAASWKTMCSDD 132
                                                                                       SFTKQARVVGGTNADEGEWPWQVSLHALGQGHLCGASLISPDWLVSAAHCFQDETIFKYS
                                                                                                                                                  DCGDGSDEASCDNVNAVSCTKYTYR-CQNGLCLNKGNPECDGKKDCSDGSDEKNCDCGLR
                                                                                                                                                                                                             FCKPLFWVCDSVN
                                                                                                                                                                                                                                                                      CPGMFMCKTG-RCIRKDLRCDGWADCPDYSDERHC-----RCNATHQFMCKNQ 499
                                                      SWTIQVGLVSLLDNPA---PSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00134; TRYPSIN_HIS; UNKNOWN_1. PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                    -SRIVGGNMSLLSQWPWQASLQFQGY-HLCGGSVITPLWIITAAHCVYDLYLPK--
                                                                                                                                                                                                                                        WKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPD------
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Protease; Serine protease
55 665 K -> N.
                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUB; 2.
ldl_recept_a; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=DUODENUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-JEJUNUM;
                                                                                                                                                                              DKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              serine
                                                                                                                                                                                                                                                                                                                                                22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                           94955 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rine protease expressed in rat small intestine."; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                              Score 542.5;
Pred. No. 3e
                                                                                                                                                                                                            GSDEEGCSCPAGSFK---CSNGKCLPQSQQCNGKD
                                                                                                                                                                                                                                                                                                                                                                                                           35806B7ECF6CF03D CRC64;
                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEASE FAMILY (S1).
                                                                                                                                                                                                                                                                                                                                                               DB 11;
                                                                                                                                                                                                                                                                                                                                 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR CLASS
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                 83;
                                                                                                                                                                                                                                                                                                                              Gaps
                                                          320
                                                                                       667
                                                                                                                                                                                                          548
                                                                                                                    266
                                                                                                                                                                              214
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PRESULT OF PROPERTY OF THE PRO
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                                                                                                                                                                                                                                                                                                                                             A BUTLIS K.C. BUSAND A. BULLER H. Caddeu E. Center A. Chandra I.,

A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A Cherry J.M., Cawley S., Dahlke C., Daven P.,

A Cherry J.M., Cawley B., Davies M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pielschmann W.,

A Dodson K.J., Doup L.E., Correll J.H., Glasser K.,

A Cherry J.M., Cawley B., Downes M., Calsart W.M., Glasser K.,

A Glodek A., Goog F., Gorrell J.H., Glu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Haskon D., Houston K.A., Howland T.J., Wei M.-H., Ibeqwam C.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McShrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McShrefi A.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resse M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Syles B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Syles B.C., Stapleton M., Strong R., Sun E.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Williams S. M. Woodley K.C., Wu D., Yang S., Yao O.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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Q9VSU2; Q9VSU1;
Q1-MAY-2000 (TrEMBLrel. 13)
01-MAR-2001 (TrEMBLrel. 16)
01-MIN-2001 (TrEMBLrel. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEQUILA OR CG4821 OR CG4948 OR CG18403. Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEQUILA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amanatides P.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pterygota; Neoptera; Endopte
Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 844
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                                   SIMILARITY: TO SIMILARITY: TO
                                                                                                                                 SIMILARITY: TO LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR CLASS
                                                                                                     (LDLRA) DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFLDWIHEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPSMLCAGYLTGGVDSCQGDSGGPLVCQER--RLWKLVGATSFGIGCAEVNKPGVYTRVT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPICLPDNTHVFPAGKAIWVTGWGHTKEG-GTGALILQKGEIRVINQTTC--EELLPQQI 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVRDWIKEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPRMMCVGFLSGGVDSCQGDSGGPLSSVEKDGRIFQ-AGVVSWGEGCAQRNKPGVYTRIP 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9600b; PHUDBELT A.C. EVANS C.A., GUCUI, S.E., CELNIKER S.E., HOLL R.A., EVANS C.A., GUCUI, S.E., P.G., SCherer S.E., Li P.W., Hoskins R.A., Galle R.E., P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E., Li P.W., Ashburner M., Henderson S.N., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Lewis S.E., Paradall M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447
TO SERINE PROTEASES, THE TO CHYMOTRYPSIN SERINE AAF50319.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endopterygota; Diptera;
¡lidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13,
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17,
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Last sequence update)
Last annotation updat
                                                                      TRYPSIN FAMILY
                                      PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fleischmann
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                                                                                                                                                                                                                                                                   H.O.,
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HSSP; P20231; 1AAO. FlyBase; FBgn0023479;

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RESULT 13
Q9U112
ID Q9U112
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R SMART; SM00192; SR; 2.

R SMART; SM00202; Tryp_SPC; 1.

R PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.

R PROSITE; PS01209; LDLRA_1; 1.

R PROSITE; PS01209; LDLRA_2; 2.

R PROSITE; PS00420; SRCR_1; UNKNOWN_2.

R PROSITE; PS00420; SRCR_2; 2.

R PROSITE; PS00434; TRYPSIN_HIS; UNKNOWN_1.

R PROSITE; PS00134; TRYPSIN_SER; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.

R Glycoprotein; Hydrolase; Serine protease.

O SEQUENCE 1186 AA; 131246 MW; 7F474D3968B8A32D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00530; SRCR; 2.
Pfam; PF00089; trypsin; 2.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR007261; LDLRECEPTOR.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR00258; SPERACTRCPTR.
                                                                              1177
                                                                                                                                                                                                         1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00057; ldl_recept_a; 2.
Pfam; PF00530; SRCR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000194; ATPase_alpha_beta.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR0012172; LDL_recept_A.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR001190; SRCR.
InterPro; IPR001254; Trypsin.
                                                                                                                                            1117
                                                                                                            446
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                                                                                                                                                                                                                                                                         997
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                                                                                                                                                                                                                                                                                                       269
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                                                                                                                                                                                                                                                                                                                                                                                                                                    207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 LRVSSLEGQFREEFVSIDHLL---PDDKVTALHHSVYVREGCASGHVVTLQCTA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 GLGIH------FDCSGKY-RCRSSFKCIELIARCDGVSDCKDGEDEYRCV
                                                                                                                                                            CAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIH
||| : |||| || :|||| :||||:
                                                                                                                                                                                                                                                                                           TIQVG--LVSLLDNPAPSHLVEKIVYHSKY-KPKRLGNDIALMKLAGPLTFNEMIQPVCL
                                                                                                            EQMERDL
                                                                                                                                                                                                                          PNSEENFPDGKVCWTSGWGATEDGAGDASPVLNHAAVPLISNKICNHRDVYGGIISPSML
                                                                                                                                                                                                                                                                                                                                     ERVVRGNVAQRGRHPWQATIRTRGRGGISSHWCGAVVISKRHLLTAAHCLYG--SPKGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GWGVHNCGVDEVAGVTCKVPVMKCPNNYWLCHTSKECIPPAFVCDNTPDCADKSDE--CA
                                                                            EKINESL
                                                                                                                                            CAGSMDESVDACEGDSGGPLVCSDDDGETLYGLISWGQHCGFKNRPGVYVRVNHYIDWIY
                                                                                                                                                                                                        PDKNAELVEDRKCTISGWGSIKSGVSTPAQVLGSAELPILADHVCKQSNVYGSAMSEGMF
                                                                                                                                                                                                                                                                     FVRVGDHYANIAESSEVDSFIENWYLHENFRKGTHMNNDIALVVLKTPLKFSDYVQPICL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIFGNSNGP-----IWLDQVMCFGNETSIDQCNHWNWGEHNCNHTEDVALHCSAGPPPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVCQAPVQYRLEGGRNSNEGRLEVKHHGVWGSVCDDDFNLKSAQVACNSMGFFGPAKIEK
                                                                                                                                                                                                                                                                                                                                                                    SRIVGGNMSLLSQWPWQASLQFQG-----YHLCGGSVITPLWIITAAHCVYDLYLPK-SW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
PRELIMINARY;
                                                                                                            452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GGQNA----VLQVFTAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.0%;
27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 539; DB 5; Pred. No. 9.9e-42;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
1449
                                                                                                                                                                                                                                                                                                                                                                                                                                ------CG------HRRGYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                       1056
                                                                                                                                                                                                                                       385
                                                                                                                                                                                                                                                                                                                                     996
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Q
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Matches 134; Conserv
                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                     SMART: SM00020; Tryp_SPC; 1.

PROSITE; PS00152; ATPASS_ALPHA_BETA; UNKNOW|
PROSITE; PS01019; LDLRA_1; 1.

PROSITE; PS00068; LDLRA_2; 2.

PROSITE; PS000420; SRCR_1; UNKNOWN_2.

PROSITE; PS000420; SRCR_2; 2.

PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_SER; 1.

GLYCOPTOCHAIN; Hydrolase; Setine protease, Sequence 1449 AA; 160045 MW; F3BC8065430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001254; Trypsin.
Pfam; PF01607; Chitin_bind_2; 2.
Pfam; PF00057; Idl_recept_a; 2.
Pfam; PF000503; SRCR; 2.
Pfam; PF000530; SRCR; 2.
Pfam; PF000530; trypsin; 1.
PRINTS; PR00725; CHYMOTRYPSIN.
PRINTS; PR007261; LDLRECEPTOR.
PRINTS; PR007261; LDLRECEPTOR.
PRINTS; PR007261; ChtBD2; 2.
SMART; SM00494; ChtBD2; 2.
SMART; SM00192; LDLa; 2.
                                                                                             1090
                                                                                                                                                          1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEQUILA OR GRAAL OR CG4821 OR CG4948 OR CG18403.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                              1145 QRYSQTQIKGGRSLGRETTPKTYSQIGLWERSSKAVHTPRRCGIFKDDLTDEYAHR---E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00202;
SMART; SM00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0023479; Tequila.
InterPro; IPR000194; Arpase_alpha_beta.
InterPro; IPR002557; Chitin_binding.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR0012172; LDL_recept_A.
InterPro; IPR001190; SRCR.
InterPro; IPR0011254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: TO SERINE PROTEASES, TI-!- SIMILARITY: TO CHYMOTRYPSIN SERINE EMBL; AJ251803; CAB64653.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          melanogaster.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
-i-SIMILARITY: TO LOW DENSITY LIPOPROTEIN (LE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09U1I2;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Munier A.I., Medzhitov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRAAL PROTEIN
                                                                                                                                                                                                                      66 GLGIH-----FDCSGKY-RCRSSFKCIELIARCDGVSDCKDGEDEYRCV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of a new serine
                                                                                                                                                                                           109
SRIVGGNMSLLSQWPWQASLQFQG----
                                                                                            NIFGNSNGP----IWLDQVMCFGNETSIDQCNHWNWGEHNCNHTEDVALHCSAGPPPRS
                                                                                                                                                                                           RV-----
                                                                                                                          LRVSSLEGQFREEFVSIDHLL----PDDKVTALHHSVYVREGCASGHVVTLQCTA-----
                                                                                                                                                          AVCQAPVQYRLEGGRNSNEGRLEVKHHGVWGSVCDDDFNLKSAQVACNSMGFFGPAKIEK 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P20231; 1AAO
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                          -GGQNA----VLQVFTAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDN
                                                                                                                                                                                                                                                                                                     22.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.,
                                                                                                                                                                                                                                                                                    74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Janeway C.,
                                                                                                                                                                                                                                                                                      Score 539; DB
Pred. No. 1.3e
74; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       protease. F3BC806543CAB6ED CRC64;
-YHLCGGSVITPLWIITAAHCVYDLYLPK-SW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRYPSIN FAMILY.
VE PROTEASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNKNOWN_1
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ease in Drosophila
                                                                                                                                                                                                                                                                                                        .3e-41;
                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBJ databases. (LDL) RECEPTO
                                                              CG-----
                                                                                                                                                                                                                                                                                                                    Length 1449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECEPTOR CLASS
                                                                                                                                                                                                                                                                                        Indels 112;
                                                            HRRGYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X
:
                                                                                                                                                                                                                                                                                      Gaps
                                                                                            1144
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                                                            214
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PERMIT OF PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
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FlyBase; FB070023479; Tequila.
InterPro; IPR000194; ATPase_alpha_beta.
InterPro; IPR00019557; Chitin_binding.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002172; LDL_recept_A.
InterPro; IPR002172; LDL_recept_A.
InterPro; IPR0019965; P_rich_extensn.
InterPro; IPR00190; SRCR.
InterPro; IPR0012965; ATPypsin.
InterPro; IPR001254; Trypsin.
Pfam; PF01607; Chitin_bind_2; 2.
Pfam; PF0057; Idl_recept_a; 2.
Pfam; PF00059; trypsin; 1.
Pfam; PF00059; trypsin; 1.
                                                                                                     SMART; SM00494; ChtBD2; 2.
SMART; SM00192; LDLa; 2.
SMART; SM00202; SR; 2.
SMART; SM00200; Tryp_SPc; 1.
PROSITE; PS00152; ATPASE ALPHA_BETA; UN
PROSITE; PS01209; LDLRA_1; 1.
PROSITE; PS01209; LDLRA_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9U1I3;
Q9U1I3;
01-MAY-2000
01-MAY-2000
  PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRAAL PROTEIN.
TEQUILA OR GRAAL OR CG4821 OR CG4948 OR CG18403.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                  PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00251; LDLEBCEPTOR.
PRINTS; PR01217; PR1CHEXTENSN.
PRINTS; PR00258; SPERACTRCPTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY -!- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAM: EMBL; AJZ51802; CAB64652.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1999) to the
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"Characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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PS00420; SRCR_1; UNKNOWN_2.
PS50287; SRCR_2; 2.
PS00134; TRYPSIN_HIS; UNKNOWN_1.
PS00135; TRYPSIN_SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999) to the EMBL/GenBank/DDBJ databases.
TO LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR
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new serine prot
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Base in Drosophila
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The state of the s

Marine Street

Query Match Best Local Similarity

22.0%;

Score Pred.

539; DB 5; No. 2.5e-41;

Length 2382;

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RESULT
Q9BI19
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Best Local :
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01-JUN-2001 (TrEMBLrel. 17
01-JUN-2001 (TrEMBLrel. 17
GRAAL2 PROTEIN PRECURSOR.
GRAAL.
Signal.
SIGNAL
SEQUENCE
                                                                                                                                                                                                                                                                                       Q9BI19;
Q9BI19;
                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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SEQUENCE 1462 AA; 161444 MW; E3AC494FE140F37A CRC64;
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                                            EMBL; AJ309005; CAC35209.1;
                                                       Submitted
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                                                       "Graal a Drosophila gene coding for several mosaic serine proteases.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                      Capovilla M., Lagueux
                                                                                                  Munier A.I., Medzhitov R., Janeway C.A.,
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            1453 EKINESL 1459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRVSSLEGQFREEFVSIDHLL---PDDKVTALHHSVYVREGCASGHVVTLQCTA-----
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2382
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  ΑĀ,
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264348 MW;
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27.5%;
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Last annotation
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 POTENTIAL.
W; 51C85282B06833D4
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No. 1.3e-41;
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                                                                                                                                                                         Brachycera; Muscomorpha;
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    CRC64;
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                                                                                                   2373 EKINESL 2379
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                                                                                                                                                                                                                                                          2253 PDKNAELVEDRKCTISGWGSIKSGVSTPAQVLGSAELPILADHVCKQSNVYGSAMSEGMF 2312
                                                                                                                                                                                                                                                                                                                                          2193 FVRVGDHYANIAESSEVDSFIENWYLHENFRKGTHMNNDIALVVLKTPLKFSDYVQPICL 2252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1963 AVCQAPVQYRLEGGRNSNEGRLEVKHHGVWGSVCDDDFNLKSAQVACNSMGFFGPAKIEK 2022
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                                                                                                                                        446 EQMERDL 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 LRVSSLEGQFREEFVSIDHLL---PDDKVTALHHSVYVREGCASGHVVTLQCTA----- 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 RV-------GGQNA---VLQVFTAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDN 155
                                                                                                                                                                                                      386 CAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIH 445
                                                                                                                                                                                                                                                                                                                                                                  269 TIQVG--LVSLLDNPAPSHLVEKIVYHSKY-KPKRLGNDIALMKLAGPLTFNEMIQPVCL 325 ::|| : || || : || || || :: :||:||
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                                                                                                                                                                                                                                                                                    PNSEENFPDGKVCWTSGWGATEDGAGDASPVLNHAAVPLISNKICNHRDVYGGIISPSML 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.4; Mismatches 167; Indels 112;
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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
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Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
 BLOSUM62
Gapop 10.0 , Gapext 0.5
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2447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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KOMSPL
KOMSPL
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PLMU
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J70172
B6156160
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1775.321 Million cell updates/sec
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enteropeptidase (E
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brain-specific ser
plasmin (EC 3.4.21
acrosin (EC 3.4.21
low-density lipopr
plasmin (EC 3.4.21
tryptase (EC 3.4.21
plasmin (EC 3.4.21
          coagulation
mast cell pr
                                                                                                                                                                                                                                                                                                           hepsin (EC 3.4.21.
                                                                                                                                                                                                                                                                                                                               Description
proteina
(EC 3.4.2
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ALIGNMENTS

Db 230 LQLGVQAVYHGGYLPFRDPNSEENSNDIALVHLSSPLPLTEYIQPVCLPAAGQALVDGK 289 Qy 337 VCWTSGWGATEDGAGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDS 396 : : :	Qy 286 LVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGK 336	OY 232 ASLOFQGYHLCGGSVITPLWIITAAHCVYDLXLPKSWTIQVGLVSLLDNPAPSH 285	Qy 177 PDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQ 231 : : :	Qy 119 VFTAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLL 176	Qy 59 LILALAIGIGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQ 118 :	Ouery Match 27.2%; Score 664.5; DB 1; Length 417; Best Local Similarity 35.7%; Pred. No. 1.5e-45; Matches 149; Conservative 62; Mismatches 143; Indels 63; Gaps	A; Gene: GDB:HPN; TMPRSSI; hepsin A; Gene: GDB:HPN; TMPRSSI; hepsin A; Gross-references: GDB:135685; OMIM:142440 A; Map position: 19q11-19q13.2 C; Superfamily: hepsin; trypsin homology C; Superfamily: hepsin; trypsin homology C; Keywords: hydrolase; liver; serine proteinase; transmembrane protein F; 23-45/Domain: transmembrane #status predicted <tmn> F; 163-400/Domain: trypsin homology <try> F; 163-400/Domain: trypsin homology <try> F; 188-204, 291-359, 322-338, 349-381/Disulfide bonds: #status predicted F; 203, 257, 353/Active site: His, Asp, Ser #status predicted</try></try></tmn>	A;Accession: S00845 A;Molecule type: mRNA A;Residues: 1-417 <ley> A;Cross-references: EMBL:X07732; NID:g32063; PIDN:CAA30558.1; PID:g32064 C;Genetics:</ley>	RESULT 1 \$00845 \$00845 hepsin (EC 3.4.21) - human C.Species: Homo sapiens (man) C.Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999 C.Accession: \$00845 R.Leytus S.P.: Loeb, K.R.; Hagen, F.S.; Kurachi, K.; Davie, E.W. Blochemistry 27, 1067-1074, 1988 A.Title: A novel trypsin-like serine protease (hepsin) with a putative transfareference number: \$00845; MUID: 88209431
ð. 15	36	35)1 77	76 22	* &	12;	·		1999 transmembrane

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A;Relecule type: protein
A;Residues: 801-807,'Y',809-827 <LIG>
A;Residues: 801-807,'Y',809-827 <LIG>
C;Comment: The mechanism of association with the membrane of the intestinal brush border embrane attachment using a signal-anchor sequence.
C;Comment: Conversion from membrane-bound to soluble forms may involve further processin C;Complex: mature enteropeptidase is variously reported to contain two (heavy and light) Lfide linked
C;Function:
A;Description: cleaves propeptide from trypsinogen to produce active trypsin
A;Pathway: intestinal digestive hydrolase cascade
C;Superfamily: enteropeptidase; Clr/Cls repeat homology; LDL receptor ligand-binding rep:
C;Keywords: glycoprotein; hydrolase; intestine; serine proteinase; transmembrane protein;
F;22-38/Domain: transmembrane #status predicted <TMM>
F;22-117/Product: enteropeptidase heavy chain #status predicted <MCH>
F;118-800/Product: enteropeptidase heavy chain #status predicted <MCH>
F;39-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;542-647/Domain: Clr/Cls repeat homology <Clr>
F;59-693/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;694-799/Domain: LDL receptor ligand-binding repeat homology *status atypical <SRC F;801-1035/Product: enteropeptidase light chain #status predicted <LCH>
F;801-1035/Product: enteropeptidase light chain #status predicted <LCH>
F;38-912,826-933,263,264,404,456,485,519,550,646,698,722,741,762,864,903,965/Bindin F;88-912,826-842,926-933,957-972,983-1011/Disulfide bonds: #status predicted
F;841,892,987/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enteropeptidase (EC 3.4.21.9) precursor bovine %,Alternate names: enterokinase C;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A43909; A48874; A61436 R:Kitamoto, Y:; Yuan, X:; Wun Q:; McCourt, D.W.; Sadler, J.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The amino-terminal sequence of the A;Reference number: A61436; MUID:92189715 A;Accession: A61436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:LaVallie, E.R.; Rehemtulla, A.; Racie, L.A.; DiBlasio, J. Biol. Chem. 268, 23311-23317, 1993
A:Title: Cloning and functional expression of a cDNA enca; Reference number: A48874; MUID:94043122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-1035 < KIT>
A; Cross-references: GB:U09859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A;Title: Enterokinase, the initiator of intestinal digestion, A;Reference number: A43090; MUID:94329561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: parts of this sequence, R;Light, A.; Janska, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:L19663; NID:g416131; PIDN:AAAA16035.1; PID:g416132
A;Note: parts of this sequence, including the amino end of the mature pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 801-1035 <LAV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: small intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A43090
                                                                                                                           Matches
      652
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                                                            66 GLGIHFDC-SGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRV----GGQNAVLQVF 120
GLGIPEPCKEDNFQCKDG-ECIPLVNLCDGFPHCKDGSDEAHCVRLFNGTTDSSGLVQFR 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CQGDSGGPLVCQE----RRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CQGDSGGPFVCEDSISRTPRWRLCGIVSWGTGCALAQKPGVYTKVSDFREWIFQAIK 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .; Janska, H.
Chem. 10, 475-480, 1991
                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid sequence not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                     27.0%;
36.9%;
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                                                                                                                        70;
                                                                                                                                           Score 660; DB 1
                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           catalytic subunit of bovine enterokinase.
                                                                                                                                                                              DB 1;
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                                                                                                                        146;
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                                                                                                                                                                                 Length 1035;
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                                                                                                                        34;
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                                                                                                                        Gaps
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                                                                                                                        15;
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A;Description: cleaves activation peptide from trypsinogen to produce A;Pathway: intestinal digestive hydrolase cascade C;Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor C;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane F;1-784/Product: enteropeptidase heavy chain #status predicted <HCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-1019 <RIT>
A; Residues: 1-1019 <RIT>
A; Cross-references: GB:U09860; NID:g746412; PIDN:AAC50138.1; F
R; Kitamoto, Y; Yuan, X; Wu, Q; McCourt, D.W; Sadler, J.E.
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A; Title: Enterokinase, the initiator of intestinal digestion,
A; Reference number: A43090; MUID:94329561
A; Accession: B43090
A; Status: nucleic acid sequence not shown
A; Status: nucleic acid sequence not shown
F:643-677/Domain: LDL receptor ligand-binding repeat homology <LDL2
F;678-783/Domain: scavenger receptor cysteine-rich domain homology
F;785-1019/Product: enteropeptidase light chain #status predicted <
F;785-1014/Domain: trypsin homology <TRY>
F;116,147,179,328,335,388,440,470,503,534,630,682,706,725,848,887,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A56318; B43090
R;Kitamoto, Y:; Veile, R.A.; Donis-Keller, H.; Sadler, J.E.
Biochemistry 34, 4562-4568, 1995
A;Title: CDNA sequence and chromosomal localization of human
A;Reference number: A56318; MUID:95234679
A;Accession: A56318
                                                                                                                                                          F;22-38/Domain: transmembrane #Status prédicted <TMM>
F;184-221/Domain: LDL receptor ligand-binding repeat l
F;342-504/Domain: MAM homology <MAM>
F;526-631/Domain: C1r/C1s repeat homology <C1R>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ducts.
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Complex: Mature enteropeptidase
ed by a disulfide bond. Possibly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:384083; OMIM:226200
A;Map position: 21q21-21q21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Comment: The mechanism of association with the membrane of the intestinal brush otated below) or with amino-terminal myristoylation of the heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:U09860 C;Comment: The mechanism of as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 749-1019
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A56318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N; Alternate names: enterokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enteropeptidase (EC 3.4.21.9)
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,534,630,682,706,725,848,887,909,949/Binding

sit

#status predicted

#status

predicted

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N'Alternate names: enterokinase
C;Species: Sus scrofa domestica (domestic pig)
C;Pate: 07-Oct-1994 #sequence_revision 09-Aug-1996 #text_change 18-Jun-1999
C;Accession: A53663
R;Matsushima, M.; Ichinose, M.; Yahagi, N.; Kakei, N.; Tsukada, S.; Miki, K.; Kurokawa, J. Biol. Chem. 269, 19976-19982, 1994
A;Title: Structural characterization of porcine enteropeptidase.
A;Reference number: A53663
A;Recession: A53663
A;Accession: A53663
A;Accession: A53663
A;Accession: A53663
A;Cross-references: GB:D30799; NID:9505122; PIDN:BAA06459.1; PID:9505123
A;Note: parts of this sequence, including the amino ends of three chains isolated from C;Comment: The mechanism of association with the membrane of the intestinal brush borde otated below) or with amino-terminal myristoylation of the heavy chain.
C;Complex: Mature enteropeptidase is variously reported to contain two (heavy and light ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms invol
C;Function:
A;Description: cleaves activation peptide from trypsinogen to produce active trypsin A;Description: cleaves activation peptide from trypsinogen to produce active trypsin A;Description: cleaves activative hydrolase cascade
C;Superfamily: enteropeptidase; Clr/Cls repeat homology; LDL receptor ligand-binding
C;Reywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymoge
F;22-38/Domain: transmembrane #status predicted <MMN>
F;52-117/Product: enteropeptidase mini chain #status predicted <MCH>
F;118-799/Product: enteropeptidase heavy chain #status predicted <HCH>
F;119-236/Domain: LDL receptor ligand-binding repeat homology <LDLl>
F;357-519/Domain: Clr/Cls repeat homology <Clr>
F;541-646/Domain: Clr/Cls repeat homology <Clr>
F;693-798/Domain: LDL receptor ligand-binding repeat homology #status atypical <F;800-1024/Product: enteropeptidase light chain #status predicted <LCH>
F;800-1029/Domain: trypsin homology <TRY>
F;116,147,170,194,283,343,350,403,455,485,518,549,645,697,701,721,740,761,804,863,902
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Pred. No. 1.7e-44;
        ,455,485,518,549,645,697,701,721,740,761,804,863,902,
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hepsin (EC 3.4.21.-) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan
C;Accession: S33777; S32013
R;Parley, D.; Reymond, F.; Nick, H.
Biochim. Biophys. Acta 1173, 350-352, 1993
A;Title: Cloning and sequence analysis of rat
A;Reference number: S33777; MUID:93305733
A;Accession: S33777
                                                                                                                                                                                                                                                                                                        C;Superfamily: hepsin; trypsin homology
C;Keywords: hydrolase; liver; serine proteinase; tran
F;22-44/Domain: transmembrane #status predicted <TMN>
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Вþ
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                                                                                                                                                                                                                                           F;162-399/Domain: trypsin homology <TRY> F;187-203,290-358,321-337,348-380/Disulfide bonds: \#status F;202,256,352/Active site: His, Asp, Ser \#status predicted
                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416. <FAR>
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Best Local S
Matches 149
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                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                             60 ILALAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQV 119
DKTEGTWRLLCSSRSNARVAGLGCEEMGFLRALAHSELDVRTAGANGTSGFFCVDEGGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNRWLLAGVTSFGYQCALPNRPGVYARVPKFTEWI 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VINPHYNRRRKDSDIAMMHLEFKVNYTDYIQPICLPEENQVFPPGRICSIAGWGKV-IYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAPNGSLILTASEQCFEDSLILLQCNHKSCGKKQVAQEVSPKIVGGNDSREGAWPWVVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSIWHTACAENWTTQTSDDVCQLLGLGTGNSSMPF-FSSGGG----PFVKLN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGIPEPCKEDNFQCENG-ECVLLVNLCDGFSHCKDGSDEAHCVRFLNGTANNSGLVQFRI 710
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                                  -FTAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSID----- 173
                                                                         VAALTVGTLLFLTGIG----AASWAIVTILLR-----SDQEPLYQVQLSPGDSRLLVL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWI 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSPADILQEADVPLLSNEKCQQQMPEYN - - ITENMMCAGYEEGGIDSCQGDSGGPLMCLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TALHHSVYV--REGCASGHVVTLQCT--ACGHR----RGYSSRIVGGNMSLLSQWPWQASL
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37.7%;
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                                                                                                                                                                        Score 645;
Pred. No. 5
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Pred. No. 3e-44;
                                                                                                                                                      Mismatches
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---HLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPW

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F;20-390/Product:
F;20-109/Domain: &
F;110-199/Domain:
                                   C;Superfamily: coagulation factor XI; trypsin homology C;Superfamily: coagulation; duplication; fibrinolysis; F;1-19/Domain: signal sequence #status predicted <SIGS-F;20-390/Product: plasma kallikrein heavy chain #status ex
                                                                                                                                                                                 A;Cross-references: GB:M58590; NID:g206721; PIDN:AAA42069.1; PID:g206722 C;Comment: This protein, synthesized in the liver, circulates as a nonco C;Comment: The zymogen is activated by factor XIIa, which cleaves the mo
                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 20-45; 391-413 <PAQ>
R; Seidah, N.G.; Ladenheim, R.; Mbikay, M.;
DNA Cell Biol. 8, 563-574, 1989
A; Title: The cDNA structure of rat plasma k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-638 <SEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasma kallikrein (EC 3.4.21.34) precursor - rat Kallikrein (RALTERNALE NAMES: Fletcher factor; kininogenin; serum kallikrein C; Species: Rattus norvegicus (Norway rat) C; Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 10; Accession: A39180; A33320; S0685; I53041; S06852 R; Beaublen, G:; Rosinski-Chupin, I; Mattei, M.G.; Mbikay, M.; Ch Biochemistry 30, 1628-1635, 1991
                                                                                                 A;Gene: PK
C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A33320;
A;Accession: A33320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: the authors translated the codon GAG for residue 81 as R;Seidah, N.G.; Ladenheim, R.; Mbikay, M.; Hamelin, J.: r.nf^{-1}1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: A39180
A;Molecule type: DNA
A;Residues: 1-638 <B
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A; Residues: 1-638 <RE
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A; Accession: I53041
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession:
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                                                                                                                                                                are linked by one or more disulfide bonds
                     20-109/Domain: apple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ah, N.G.; Ladenheim, R.;
563-574, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDSGGPLVCQER----RLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVTGWGNTQ-FYGQQAVVLQEARVPIISNEVCNSPDFYGNQIKPKMFCAGYPEGGIDACQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDSGGHFVCEDRISGTSRWRLCGIVSWGTGCALARKPGVYTKVIDFREWIFQAIK
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                                                                                                                                                                                                                                              1-638 <RES>
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                     repeat <AP1>
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MUID:90091743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NID:g205010; PIDN:AAA41463.1; PID:g205011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamelin, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NH(2)-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ends of both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chretien,
                                      experimental <MAT1>
                                                                                                                                                                                                                                                                                                                                                                                     Lutfalla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lutfalla,
                                                                              glycoprotein; hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequencing
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                                                                                                                                                                                                      noncovalent
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132 DWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHHSVYVR 191

Query Match Best Local S Matches 126

Local Similarity hes 126; Conser

Conservative

61;

Pred. No. 4.76 L; Mismatches

Indels

66;

Gaps

12;

561; No. 4

DB 1; .7e-37;

22.9%;

Score

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F:110-199/Domain: apple repeat <AP2>
F;200-289/Domain: apple repeat <AP3>
F;291-380/Domain: apple repeat <AP4>
F;391-638/Product: plasma kallikrein light chain #status experimental <LCH>
F;391-621/Domain: trypsin homology <TRY>
F;391-621/Domain: trypsin homology <TRY>
F;211-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,
F;127,215,308,396,494/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;434,483,578/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                     are linked by one or more disulfide bonds.

(Superfamily: coagulation factor XI; trypsin homology C; Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-390/Product: plasma kallikrein heavy chain #status experimental <HCH>
F;20-199/Domain: apple repeat <APl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasma kallikrein (EC 3.4.21.34) precursor
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1992 #sequence_revision 30-S
C;Accession: A36557
R;Seidah, N.G.; Sawyer, N.; Hamelin, J.; Mi
                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M58588; NID:g200358; PIIN:AAA63393.1; PID:g200359
A;Note: part of this sequence, including the amino ends of both the heavy and light C;Comment: This protein, synthesized in the liver, circulates as a noncovalent compl C;Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-638 <SEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;391-638/Product: plasma kallikrein light chain #status experimental <MAT2>
F;391-621/Domain: trypsin homology <TRY>
F;21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Mouse plasma kallikrein: cDNA structure,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 LVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQM----ERDLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 YHLCGGSVITPLWIITAAHCVYDLYLPKSWT QVGLVSL--LDNPAPSHLVEKIVYHSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 YVREGCASGHVVTL-----QCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQ---G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVGITSWGEGCARKEOPGVYTKVAEYIDWILEKIOSSKERALET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNHAAVPLISNKIC--NHRDVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KMSEGSYDIALIKLQTPLNYTEFQKPICLPSKADTNTIYTNCWVTGWGYTKE-RGETQNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NHMCGGSIIGRQWILTAAHCFDGIPYPDVWRIYGGILNLSEITNKTPFSSIKELIIHQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEAQG-SSGYSLRLCKVVESSDCTT-----KINARIVGGTNSSLGEWPWQVSLQVKLVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQKATIPLVPNEECQKKYRDY---VITKQMIÇAGYKEGGIDACKGDSGGPLVCKHSGRWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beaubien, G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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(covalent) #status experimenta

#status

predicted

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A;Gene: GDB:IXLK3

A;Cross-references: GDB:127575; OMIM:229000

A;Map position: 4q35-4q35

C;Superfamily: coagulation factor XI; trypsin homology
C;Superfamily: coagulation; duplication; fibrinolysis; glycc
F;1-19/Domain: slynal sequence #status predicted <SIG>
F;20-638/Product: plasma kallikrein #status predicted <MAT>
F;20-390/Domain: apple repeat <AP1>
F;20-199/Domain: apple repeat <AP2>
F;110-199/Domain: apple repeat <AP3>
F;20-289/Domain: apple repeat <AP3>
F;20-1-80/Domain: apple repeat <AP3>
F;21-180/Domain: apple repeat ilight chain #status predicte
F;391-638/Domain: plasma kallikrein light chain #status predicte
F;391-631/Domain: trypsin homology <MRY>
F;21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Human plasma pro
A;Reference number: A009;
A;Reference number: M00921
A;Molecule type: mRNA
A;Residues: 1-638 <CHU>
                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 20-27;40-46,'x',48,'H';50,'x',52-70,'H';75-76,'x',78-80;103-113;131-140;141-
260-283,'x',285;287-291,'x',293-295;314-317,'x',319-320;321-324;'x',329-333;334-339,'x'
255;538-551;562,'x',564-567;573,'x',575-576;578-583,'x',585;592-604 <mcm>
C; Comment: This protein, synthesized in the liver, circulates as a noncovalent complex w
C; Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a li
are linked by one or more disulfide bonds.
C; Comment: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It activates, in a reciprocal r
lnogen and may also play a role in the renin-angiotensin system by converting prorenin i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M13143; NID:g190262; PIDN:A R;MCMullen, B.A.; Fujikawa, K.; Davie, E.W. Biochemistry 30, 2050-2056, 1991
A;Title: Location of the disulfide bonds in human A;Reference number: A37939; MUID:91152016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasma kallikrein (EC 3.4.21.34) precursor - human N;Alternate names: kininogenin; plasma prekallikrein C;Species: Homo sapiens (man) C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999 C;Accession: A00921; A37939 R;Chung, D. M.; Fujikawa, K.; McMullen, B.A.; Davie, E.W. Biochemistry 25, 2410-2417, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QY
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A00921; MUID:86243359
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     ,141-147,201-284,227-256,231-237,292-375,
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                                                       #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
     580
                                      403
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                                      GPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHEQME
                                                                                                                                                                                                                                                                                                                                                        DFGGEELNV-----TFVKGVNVCQETCTKMIRCQFFTYS-LLPEDCKEEKCKCFLRL
                                                                                                                                                                                                                                                                                                                                                                                           DWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDD----
GPIVCKHNGMWRLVGITSWGEGCARREQPGVYTKVAEYMDWILEKTQ
                                                                         GFSKE-KGEIQNILQKVNIPLVTNEECQKR--
                                                                                           GATEDGAGDASPYLNHAAVPLISNKICNHRDVYGGI-ISPSMLCAGYLTGGVDSCQGDSG
                                                                                                                                                                                                                                                                                                                    ----KVTALHHSVYVREGCASGHVVTL-----QCTACGHRRGYSSRIVGGNMSLLSQW
                                                                                                                                             FSQIKEIIIHQNYKVSEGNHDIALIKLQAPLNYTEFQKPICLPSKGDTSTIYTNCWVTGW
                                                                                                                                                                            SHLVEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGW
                                                                                                                                                                                                                 PWQVSLQVKLTAQRHLCGGSLIGHQWVLTAAHCFDGLPLQDVWRIYSGILNLSDITKDTP
                                                                                                                                                                                                                                                PWQASLQFQ---GYHLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLD--NPAP
                                                                                                                                                                                                                                                                                    SMDGSPTRI---AYGTQG-SSGYSLRLCNTGDNSVCTT----KTSTRIVGGTNSSWGEW
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                                                                                                                                                                                                                                                                                                                                                                                                                              57;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 540; DB 1;
Pred. No. 2.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                         YQDYKITQRMVCAGYKEGGKDACKGDSG
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                                      449
   626
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                                                                                                        402
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                                                                                                                                                                                                                                                                                    402
                                                                                                                                                                                                                                                                                                                                                        351
                                                                                                                                                                                                                                                  283
                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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plasmin (EC 3.4.21.7) precursor - pig (fragment)

N;Alternate names: plasminogen

N;Contains: miniplasminogen

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997

C;Accession: S03733; S03737; A25834

R;Schaller, J; Marti, T; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.

Fibrinolysis 1, 91-102, 1987

A;Title: Amino acid sequence of the heavy chain of porcine plasmin. Compari:
A;Reference number: S03733
A;Accession: S03733
A;Accession: S03733
R:Marti, T.: Schaller, J.; Rickli, E.E.
Eur. J. Biochem. 149, 279-285, 1985
A;Title: Determination of the complete amino-acid
A;Reference number: A25834; MUID:85203907
A;Accession: A25834
A;Molecule type: protein
A;Residues: 450-790 <MAR>
                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 1-560 <SCH>
A; Residues: 1-560 <SCH>
R; Brunisholz, R.A.; Lerch, P.G.; Schaller, J.
Eur. J. Biochem. 114, 465-470, 1981
A; Title: Comparison of the primary structure
A; Reference number: 803735; MUID:81212097
A; Accession: S03737
                                                                                                                                                                                                A; Molecule type: protein A; Residues: 1-57 < BRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chain of porcine plasmin. Comparison
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                                                                                                                                                                                                                                                                                                                                                             Rickli,
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                                                                                                            porcine
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                                                                                                            miniplasminogen
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urokinase-type

plasminogen

factor

in

proteolytic

kringle;

(fragment)

protein precu ingle; plasma;

serine

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A;Experimental source: brain
C;Superfamily: brain-specific serine proteinase; scavenger receptor cysteine-rich domain
C;Superfamily: brain-specific serine proteinase
E;Be-157/Domain: kringle-like #status predicted <KRI>
F;B3-266/Domain: kringle-like #status predicted <KRI>
F;163-266/Domain: scavenger receptor cysteine-rich domain homology <SRC7>
F;166-266,273-372,386-486/Domain: scavenger receptor cysteine-rich #status predicted <SF
F;513-515/Domain: furin binding #status predicted <FRB>
F;517-755/Domain: trypsin homology <TRY>
F;517-755/Domain: trypsin homology <TRY>
F;93,521,569/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;562,612,711/Active site: His, Asp, Ser #status predicted
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F;84-162/Domain: kringle homology <KR1>
F;166-243/Domain: kringle homology <KR2>
F;256-333/Domain: kringle homology <KR3>
F;358-435/Domain: kringle homology <KR3>
F;358-435/Domain: kringle homology <KR4>
F;450-790/Product: miniplasminogen *status experimental <MIN>
F;461-540/Domain: kringle homology <KR5>
F;561-790/Product: plasmin chain B *status experimental <BCH>
F;561-780/Domain: trypsin homology <TRY>
F;561-783/Domain: tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Yamamura, Y.; Yamashiro, K.; Tsuruoka, N.; Nakazato, H.; Tsujimura, A.; Yamaguchi, N. Biochem. Biophys. Res. Commun. 239, 386-392, 1997
A;Title: Molecular cloning of a novel brain-specific serine protease with a kringle-like A;Reference number: JC5759; MUID:98008848
A;Accession: JC5759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brain-specific serine proteinase (EC 3.4.21.-) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 31-Mar-2000
C;Accession: JC5759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
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A; Residues: 1-761 < YAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bonds: #status predicted
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Best Local
                                                                                                                                                                           Matches
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326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428 VNKPGVYTRVTSFLDWIHEQMERD 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252
                                                                                                                                                                                                               Local
                                                                                     70 HFD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGKPKVEPKKCPA------RVVGGCVSIPHSWPWQISLRYR-YRGHFCGGTLISPEW
HFDGSNRPIWLDDVSCSGK---EVSF--IQCSRRQWGRHDCSHREDVGLTCYPDSDGHRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKI--VYHSKYKPKRLGNDIALMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNKPGVYVRVSRFVTWIEEIMRRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSSPAVITDKVIPACLPTPNYVVADRTACYITGWGETKGTYGAG----LLKEARLPVIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATED--GAGDASPVLNHAAVPLISN
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                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                   -----CSGKYRCRSSFKCIELIARCDGVSDCKDGED----
                                                                                                                                                                                                      21.4%;
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Pred. No. 3.8e-34;
42; Mismatches 86
                                                                                                                                                                  Score 523.5; DB 2;
Pred. No. 5.8e-34;
3; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 790
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C.Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol C.Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase F;1-33,34-117,118-45/Product: plasminogen (fragments) #status experimental <PRO> F;1-33/Domain: activation peptide (fragment) #status experimental <APT> F;34-117,118-225,226-455/Product: plasmin (fragments) #status experimental <AMT> F;37-114/Domain: kringle homology <KR4> F;37-114/Domain: kringle homology <KR4> F;118-455/Product: miniplasminogen #status experimental <MIN> F;126-205/Domain: kringle homology <KR5> F;226-445/Domain: kringle homology <KR5> F;226-448/Domain: kringle homology <KR5> F;226-448/Domain: trypsin homology <KR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
A61545
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                                                          Qy
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A; Residues: 1-33,34-117 <SCH>
R; Schaller, J.; Straub, C.; Kaempfer, U.;
Protein Seq. Data Anal. 4, 69-74, 1991
A; Title: Complete amino acid sequence of
A; Reference number: S17527; MUID: 92052077
A; Accession: S17527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzyme 40, 63-69, 1988
A;Title: Structural aspects of the plasminogen
A;Reference number: A61545; MUID:89005015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Schaller, u., ...
R0, 63-69,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Equus caballus (domestic horocompate: 28-Oct-1994 #sequence_revision C;Accession: A61545; S17527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                  F;226-448/Domain: trypsin homology <TRY>F;267,310,405/Active site: His, Asp, Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmin (EC 3.4.21.7) precurso N; Alternate names: plasminogen
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A; Residues: 118-455 <SC2>
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204 QCESSPFDCGKPKVEPKKCSGRIVGGCVAIAHSWPWQISLRTRFGRHFCGGTLISPEWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              713 GPLMCEKPDESWVVYGVTSWGYGCGVKDTPGVYTRVPAFVPWI 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346
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                                     QCTA----CG----HRRGYSSRIVGGNMSLLSQWPWQASLQFQ-GYHLCGGSVITPLWII 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEDGAGDA-SPYLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYL--TGGVDSCQGDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T----GRAYSRTLQQAAVPLLPKRFCKER--YKGLFTGRMLCAGNLQEDNRVDSCQGDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YHSKYKPKRLGNDIALMKLAGP----LTFNEMIQPVCLPNSEENFPD--GKVCWTSGWGA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSCWVLTAAHCFKRYGNNSRSYAVRVGDYHTLVPEEFEQEIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J.; Rickli, E.E.
53-69, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           miniplasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.4.21.7) precursor
                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --VSSDNLRVSSLEGQFREEFVSIDHILPDDKVTALHHSV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         caballus (domestic horse)
                                                                                                                                                           21.3%;
                                                                                                                        Score 520.5; DB 2;
Pred. No. 5.5e-34;
Nismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            horse (fragments)
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QΥ

TAAHCVYDLYLPKSWTTQVGLVSLLDNPAPSHLVEKTVYHSKYKPKRLGNDIALMKLAGP

Gaps

7;

425

786

670

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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 22-27 <LIZ>
A; Residues: 22-27 <LIZ>
C; Comment: Plasminogen is synthesized by the kidney and is present in plasma and m C; Comment: Plasminogen is converted into plasmin by plasminogen activators, both p mediately after dissociation from the clot. In the presence of the inhibitor, the e inhibitor, the activation involves also removal of the activation peptide.
C; Comment: Stromelysin 1 (see PIR: KCMSS1) acts on plasminogen to produce angiostate eful in treating solid tumors.
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:J04766; NID:g200402; PIDN:AAA50168.1; PID:g2 R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D. Eur. J. Biochem. 224, 863-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system. A;Reference number: S48202; MUID:95010076
A;Accession: S48202
A;Molecule type: protein A;Residues: 20-25 <LIJ>A;Accession: S48203
A;Accession: S48203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Access.c.... G:Access.c.... SJ.F.; Bell, S.M.; Schaeter, ...... Genomics 8, 49-61, 1990
A;Title: Characterization of the cDNA coding A;Title: A38514; MUID:91184812
                                                                                                                                                                                                                                   F:20-96/Domain: activation peptide #status predicted <APT>
F:79-466/Product: angiostatin #status predicted <AST>
F:79-466/Product: angiostatin #status predicted <AMAT>
F:97-581,582-812/Product: plasmin #status predicted <MAT>
F:97-81/Domain: chain A #status predicted <ACH>
F:103-181/Domain: kringle homology <KR1>
F:103-181/Domain: kringle homology <KR2>
F:185-262/Domain: kringle homology <KR3>
F:377-454/Domain: kringle homology <KR3>
F:481-560/Domain: kringle homology <KR3>
F:481-560/Domain: kringle homology <KR5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: angiogenesis inhibitor; blood; duplication; fibri
F;1-96/Domain: plasminogen-related protein precursor homology
F;1-91/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homologyserors anglogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; E;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmin (EC 3.4.21.7) precursor - mouse
N;Contains: angiostatin; plasminogen
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
                 F;136,308/Binding site: carbohydrate (Asn) (covalent) #status predicted F;466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted F;581-582/Cleavage site: Arg-Val (plasminogen activator) #status experi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
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                                                                                              F;78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted
                                                                                                                                                                              F;582-805/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F; 20-812/Product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ns the walls of the graafian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: dissolves the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-812 <DEG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: A38514; S48202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                                                                                                                                ;582-812/Domain: chain B #status predicted <BCH>;582-805/Domain: trypsin homology <TRY>;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: A38514
           5-467/Cleavage site:
1-582/Cleavage site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434
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                                                                                                                            #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIITQNVIPACLPPADYVVANWAECFVTGWGETQDSSN--AGVLKEAQLPVIENKVCNRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLNHAAVPLISNKICNHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasminogen #status predicted <PRO>
           Thr-Val
Arg-Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibrin of blood clots; acts as a proteolytic follicle; also activates the urokinase-type p
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              (plasminogen
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              activator)
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           experimental
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F:43-286/Domain: trypsin homology <TRY>
F:44-437/Domain: acrosin heavy chain #status predicted <HCH>
F:22,211/Binding site: carbohydrate (Asn) (covalent) #status
F:25-155,29-163/Disulfide bonds: #status predicted
F:74-90/Disulfide bonds: #status predicted
F:89,143,241/Active site: His, Asp, Ser #status predicted
F:178-247/Disulfide bonds: #status predicted
F:210-226/Disulfide bonds: #status predicted
F:237-267/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                  A; Molecule type: DNA; mRNA
A; Rosidues: 1-254, 'LCDR', 259, 'DHEL', 264, 'GRLC', 269-437 < KRE>
A; Rosidues: 1-254, 'LCDR', 259, 'DHEL', 264, 'GRLC', 269-437 < KRE>
A; Note: sequence modified after extraction from NCBI backbone
A; Note: sequence extracted from NCBI backbone (NCBIN:89436, NCC; Superfamily: acrosin; trypsin homology
C; Keywords: glycoprotein; hydrolase; serine proteinase; sperm; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-43/Domain: acrosin light chain #status predicted <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Seq. 2, 57-60, 1991
A;Title: Exon intron structure and nucleotide sequence
A;Reference number: A56620; MUID:92199245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; NoLecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-254, 'LCDR', 259, 'DHEL', 264, 'GRLC', 269-437 <KLE2>
A; Residues: 1-254, 'LCDR', 259, 'DHEL', 264, 'GRLC', 269-437 <KLE2>
A; Cross references: EMBL: X59254; NID: 957282; PIDN:CAA41947.1;
R: Kremling, H.; Flake, A.; Adham, I.M.; Radtke, J.; Engel, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Contains: proacrosin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-
C;Accession: $18407; $30037; A56620
R;Klemm, U.; Flake, A.; Engel, W.
Biochim. Biophys. Acta 1990, 270-272, 1991
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S18407
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A; Accession: S30037
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A;Title: Rat sperm acrosin:
A;Reference number: S18407;
A;Accession: S18407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X59254 R;Klemm, U.; Flake, A.; Engel, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acrosin (EC 3.4.21.10) precursor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A56620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-437 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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MUID:92031708
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Pred. No. 1.
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NCBIN:89447

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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1113 <TOM>
A;Residues: 1-1113 <TOM>
A;Coross-references: DDBJ:AB013874; NID:g3869144; PIDN:BAA34371.1; PID:g3869145
C;Superfamily: trypsin homology; LDL receptor ligand-binding repeat homology <LDLL>
F;373-7372/Domain: LDL receptor ligand-binding repeat homology <LDLL>
F;374-408/Domain: LDL receptor ligand-binding repeat homology <LDLS>
F;410-445/Domain: LDL receptor ligand-binding repeat homology <LDLS>
F;447-482/Domain: LDL receptor ligand-binding repeat homology <LDLS>
F;648-682/Domain: LDL receptor ligand-binding repeat homology <LDLS>
F;684-720/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;684-720/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;733-757/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;733-757/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;869-1097/Domain: trypsin homology <TRY>
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C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1990 #sequence_revision 16-Jul-1991 #sequence_revision 16-Jul-1998 #sequence_revision 16-Jul-1999 #seq
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Species: Mus musculus (house mouse);
Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 18-Aug-2000;
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Best Local
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                                                                                                                                       TLQELLVYRHSCPSRSEISLLCSKQDCGRRPAARMNKRILGGRTSRPGRWPWQCSLQSEP
                                                                                                                                                                                                          ALHHSVYVREGCASGHVVTLQCTA--CGHRRG--YSSRIVGGNMSLLSQWPWQASLQFQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 506; DB
Pred. No. 2.2e
76; Mismatches
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Pred. No. 6.3e-33;
6; Mismatches 89;
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.2e-32;
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R; Softrup-Jensen, L.; recessions submitted to the Atlas, Jul submitted to maker: A00929
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A;Experimental source: leukocyte; lung fibroblast
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A;Reference number: A35229; MUID:90202879
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A;Title: Comparison of the primary structure of
A;Reference number: S03735; MUID:81212097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-471, 'D', 473-810 <FOR>
A; Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531
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C;Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000
C;Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000
C;Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627;
D:Daferson. T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
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PLHU
                                                                                          A; Molecule type: protein A; Residues: 20-71, 'E', 73
                                                                                                                                                   A; Reference number: A; Accession: S03735
                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 367-419 <MAL3>
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A; Residues: 292-471, 'D', 473-810 <MAL2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: liver R; Malinowski, D.P.; Sadler, J.E.; Davie, Biochemistry 23, 4243-4250, 1984
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N;Alternate names: plasminogen precursor [misnomer]
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A; Residues: 1-810 < PET>
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                                 ,'E',73-76 <BRU>
L.; Petersen, T.E:;
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                                                                  Magnusson,
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J.; Rickli, E.E.;
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Larsson, K.; Heden, L.O.
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A:Contents: annotation
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A;Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding
A;Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding
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                                                                                           submitted to the Brookhaven Protein
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                                                                                                                                                                  A; Reference number: A51911; PDB:1PKR
                                                                                                                                                                                      submitted to the Brookhaven Protein Data Bank,
                                                                                                                                                                                                                 R; Wu,
                                                                                                                                                                                                                                   A; Contents: annotation; X-ray crystallography,
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A; Residues: 483-507, 'E'
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B:, Wallen, P.
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                                                                                                                   Tulinsky,
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    1.9 angstroms,

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December 1995
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                                                                                                                                       2.48 angstroms,
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rg-580, resulting in two chains connected by two disulfide bonds. Without C:Comment: Microplasmin is formed by autolytic cleavage of plasmin under C:Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce ting solid tumors.
                                                                                         C; Keywords: anglogenesis inhibitor; blood; duplication; fibrinolysis; F;1-95(Domain: plasminogen-related protein precursor homology <PLPH>F;1-95(Domain: signal sequence #status predicted <SIG>F;20-810/Product: plasminogen #status experimental <PRO>F;20-96/Domain: activation peptide #status experimental <APT>F;20-96/Product: anglostatin #status experimental <AST>F;97-580/581-810/Product: plasmin #status experimental <AST>F;97-580/581-810/Product: plasmin #status experimental <AST>F;97-580/Domain: plasmin chain A #status experimental <CHA>F;97-580/Domain: plasmin chain A #status experimental <CHA>F;101-181/Domain: plasmin chain A #status experimental <CHA>F;101-181/Domain: kringle homology <FRIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Contents: annotation; conformation by (1)H-NMR C;Comment: Plasminogen is synthesized by the kidney and is C;Comment: Plasminogen is converted to plasmin by plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Rejante, M.; Llinas, M. submitted to the Brookhaven Protein Data A;Reference number: A65803; PDB:1HPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 30, 10589-10594, 1991
A; Title: The refined structure of the epsilon-aminocaproic acid complex of human plas A; Reference number: A58818; MUID:92031503
F; 275-352/Domain: F; 377-454/Domain:
                                                                                                                                                                                                                                                                                                                A; Pathway: fibrinolysis
C; Superfamily: plasmin; kringle homology; plasminogen-related protein
                                                                                                                                                                                                                                                                                                                                                                             A; Description: dissolves the ns the walls of the graafian
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:119498; OMIM:173350
A;Map position: 6q26-6q27
A;Introns: 17/1; 62/2; 98/1; 136/2; 183/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Rejante, M.R.; Llinas, M. Eur. J. Biochem. 221, 939-949, 1994
A;Title: Solution structure of the epsilon-aminohexanoic A;Reference number: A58817; MUID:94237158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eur. J. Biochem. 221, 927-937, 1994
A; Title: (1)H-NMR assignments and secondary structure of human plasminogen
A; Reference number: $43645; MUID:94237157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the Brookhaven Protein Data Bank, August 1996 A; Reference number: A65804; PDB:1HPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 31, 270-279, 1992
A;Title: Crystal structure of the kringle 2 domain of tissue
A;Reference number: A39483; MUID:92118803
                                                       F;185-262/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Function:
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                                                                              F;103-181/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  annotation
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                                                                              homology
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le bonds. Without
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                                                                                                                                              429 NKPGVYTRVTSFLDWIHEQMERD 451
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788 NKPGVYVRVSRFVTWIEGVMRNN 810
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